

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 20, 2005, 17:41:40 ; Search time 442 Seconds
(without alignments)
294.648 Million cell updates/sec

Title: US-10-848-737-1

Perfect score: 22
Sequence: 1 gugaacucacugagucutt 22

Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 4390206 seqs, 2959870667 residues

Word size : 0

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 300 summaries

Database : N_Geneseq_16Dec04:*

- 1: Geneseq1980s:*
- 2: Geneseq1990s:*
- 3: Geneseq2000s:*
- 4: Geneseq2001as:*
- 5: Geneseq2001bs:*
- 6: Geneseq2002as:*
- 7: Geneseq2002bs:*
- 8: Geneseq2003as:*
- 9: Geneseq2003bs:*
- 10: Geneseq2003cs:*
- 11: Geneseq2003ds:*
- 12: Geneseq2004as:*
- 13: Geneseq2004bs:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	90.9	29751	12	ADJ39000 SARS coro
2	16	72.7	619	10	Adk58384 Plant DNA
3	16	72.7	619	10	Adk57664 Plant DNA
4	16	72.7	619	11	Adm45449 Insect re
5	16	72.7	672	11	Adm44886 Insect re
6	16	72.7	686	10	Adk57646 Plant DNA
7	16	72.7	686	10	Adk54332 Plant DNA
8	16	72.7	696	11	Adm45452 Insect re
9	15	68.2	534	6	ABN69216 Streptoco
10	15	68.2	537	8	ACA50276 Prokaryot
11	15	68.2	627	6	ABN61473 Prostata
12	15	68.2	1101	13	Adr61500 Cotton cd
13	15	68.2	1191	5	ABAI14473 Human ner
14	15	68.2	1191	5	ABAI14472 Human ner
15	15	68.2	1820	4	AAI22168 Probe #12
16	15	68.2	1820	4	ABA67247 Human foe
17	15	68.2	1820	4	AAI47467 Probe #16
18	15	68.2	1820	4	ABA49335 Human bre
19	15	68.2	1820	4	ABA34342 Probe #12
20	15	68.2	1820	4	AAK15686 Human bra

C	21	15	68.2	1820	5	AAI07869	Aai07869	Probe #78
C	22	15	68.2	1820	6	ABSI5429	AbSI5429	Human gen
C	23	15	68.2	1870	4	AAI24124	Aai24124	Probe #14
C	24	15	68.2	1870	4	ABA69247	AbA69247	Human foe
C	25	15	68.2	1870	4	AAI49420	Aai49420	Probe #18
C	26	15	68.2	1870	4	ABA51239	AbA51239	Human bre
C	27	15	68.2	1870	4	ABA36163	AbA36163	Probe #14
C	28	15	68.2	1870	4	AAK43349	AaK43349	Human bon
C	29	15	68.2	1870	4	AAK17541	AaK17541	Human bra
C	30	15	68.2	1870	6	ABSI7430	AbSI7430	Human gen
C	31	15	68.2	1966	4	AAI12930	Aai12930	Probe #28
C	32	15	68.2	1966	4	ABA54631	AbA54631	Human foe
C	33	15	68.2	1966	4	AAI34291	Aai34291	Probe #29
C	34	15	68.2	1966	4	ABA44181	AbA44181	Human bre
C	35	15	68.2	1966	4	ABA44181	AbA44181	Human bre
C	36	15	68.2	1966	4	AAK02920	AaK02920	Human bra
C	37	15	68.2	1966	5	AAI02849	Aai02849	Probe #28
C	38	15	68.2	1966	6	ABN02874	AbN02874	Human gen
C	39	15	68.2	2394	10	ADC37626	AdC37626	Human nuc
C	40	15	68.2	4064	4	ABL01842	AbL01842	Drosophil
C	41	15	68.2	4064	4	ABL03058	AbL03058	Drosophil
C	42	15	68.2	4089	4	ABL04554	AbL04554	Drosophil
C	43	15	68.2	4317	13	ADR14707	AdR14707	Human NF-
C	44	15	68.2	43599	6	ABK84242	AbK84242	Human cDN
C	45	14	63.6	325	2	AAI19998	Aai19998	Human gen
C	46	14	63.6	348	6	ABN92664	AbN92664	Staphyloc
C	47	14	63.6	348	13	ADS01314	AdS01314	Staphyloc
C	48	14	63.6	534	6	ABN69215	AbN69215	Streptoco
C	49	14	63.6	1240	3	ABN53227	AbN53227	Arabidops
C	50	14	63.6	1278	13	ADT45310	AdT45310	Bacterial
C	51	14	63.6	1341	4	AAF28159	Aaf28159	Rice cent
C	52	14	63.6	1860	13	ADS16656	AdS16656	B. hensel
C	53	14	63.6	2350	10	ADE55033	AdE55033	Rat gene
C	54	14	63.6	2350	10	ADE55037	AdE55037	Rat gene
C	55	14	63.6	2457	10	ACF70959	AcF70959	Photorhab
C	56	14	63.6	3170	4	AAH54485	AaH54485	S. epider
C	57	14	63.6	3504	10	ADB69029	AdB69029	C. neofor
C	58	14	63.6	4314	8	ACA46888	AcA46888	Prokaryot
C	59	14	63.6	4323	5	AAH79450	AaH79450	DNA encod
C	60	14	63.6	4329	4	AAH53329	AaH53329	S. epider
C	61	14	63.6	9342	4	ABL02454	AbL02454	Drosophil
C	62	14	63.6	18895	13	ADS16655	AdS16655	B. hensel
C	63	14	63.6	47493	9	ADA02549	AdA02549	Mouse Wnt
C	64	14	63.6	47493	10	ADB72287	AdB72287	Mouse Wnt
C	65	14	63.6	47493	10	ADB95797	AdB95797	Mouse Wnt
C	66	14	63.6	76180	13	ABD33385	AbD33385	Human can
C	67	14	63.6	76698	12	ADJ84182	AdJ84182	Human c-r
C	68	14	63.6	110000	4	AAI99682_07	AAI99682_07	Continuation (8 of
C	69	14	63.6	110000	4	AAI99683_07	AAI99683_07	Continuation (8 of
C	70	14	63.6	110000	6	ABN71527_00	AbN71527_00	Streptoco
C	71	14	63.6	110000	10	ACF67367_40	AcF67367_40	Continuation (41 o
C	72	14	63.6	110000	10	ACF65388_07	AcF65388_07	Continuation (8 of
C	73	14	63.6	190000	10	ADL13752	AdL13752	Osteoearth
C	74	14	63.6	247544	12	ADQ59419	AdQ59419	Human can
C	75	13	59.1	21	6	ABA04625	AbA04625	MOL3 reve
C	76	13	59.1	21	10	ADJ87878	AdJ87878	G-coupled
C	77	13	59.1	21	12	ADN38524	AdN38524	Novel hum
C	78	13	59.1	190	2	AAQ76533	AaQ76533	Human gen
C	79	13	59.1	200	12	ACH89259	AcH89259	Human gen
C	80	13	59.1	240	11	ACH94421	AcH94421	Klebsiell
C	81	13	59.1	304	10	ADC72386	AdC72386	DNA Seq I
C	82	13	59.1	305	6	ABV88798	AbV88798	Human col
C	83	13	59.1	319	6	ABN19496	AbN19496	Human ORF
C	84	13	59.1	413	12	ADP95241	AdP95241	Cotton ex
C	85	13	59.1	438	3	AAH92241	AaH92241	N. mening
C	86	13	59.1	445	6	ABV97902	AbV97902	Human pan
C	87	13	59.1	478	4	ABA57952	AbA57952	Human foe
C	88	13	59.1	478	4	AAI37549	Aai37549	Probe #62
C	89	13	59.1	478	4	AAK31673	AaK31673	Human bon
C	90	13	59.1	478	4	AAK06027	AaK06027	Human bra
C	91	13	59.1	478	4	ABSI1357	AbSI1357	Human liv
C	92	13	59.1	478	6	ABN06429	AbN06429	Human gen
C	93	13	59.1	486	9	ACH20490	AcH20490	Human adu

C 94	13	59.1	539	4	AAK91848	Aak91848 Human cdn	167	13	59.1	2077	2	AAV90767	Aav90767 Nucleotid
C 95	13	59.1	539	4	AAK93253	Aak93253 Human cdn	168	13	59.1	2105	8	ABT120603	Abt120603 Aspergill
C 96	13	59.1	539	12	ADL28275	Adl28275 5' end of	169	13	59.1	2105	8	ABT18787	Abt18787 Aspergill
C 97	13	59.1	539	12	ADL29680	Adl29680 5' end of	170	13	59.1	2160	13	ADR03843	Adr03843 Carotenoi
C 98	13	59.1	570	12	ACH75524	Ach75524 Human gen	171	13	59.1	2160	13	ADR03923	Adr03923 Method of
C 99	13	59.1	584	3	AAC35392	Aac35392 Arabidops	C 172	13	59.1	2418	6	ABZ13067	Abz13067 Arabidops
100	13	59.1	585	6	ABZ13833	Abz13833 Arabidops	C 173	13	59.1	2418	8	ADA68438	Ada68438 Arabidops
101	13	59.1	603	10	ADK60004	Adk60004 Plant DNA	C 174	13	59.1	2466	2	AAV90893	Aav90893 Nucleotid
C 102	13	59.1	625	6	ABV96002	Abv96002 Human pan	C 175	13	59.1	2518	4	AAK94748	Aak94748 Human ful
C 103	13	59.1	646	6	ABV99049	Abv99049 Human pan	C 176	13	59.1	2518	12	ADL31785	Adl31785 Full leng
C 104	13	59.1	678	4	AAV53311	Aav53311 Haemophil	C 177	13	59.1	2555	12	ADQ23265	Adq23265 Human sof
C 105	13	59.1	678	8	ACA34154	Aca34154 Prokaryot	C 178	13	59.1	2571	13	ADR07375	Adr07375 Full leng
106	13	59.1	709	10	ADK56318	Adk56318 Plant DNA	C 179	13	59.1	2795	2	AAT97609	Aat97609 Human E2A
C 107	13	59.1	714	10	ADQ92613	Adq92613 Human col	C 180	13	59.1	2892	8	ACA24242	Aca24242 Prokaryot
C 108	13	59.1	796	6	ABN99064	Abn99064 Arabidops	C 181	13	59.1	2916	13	ADR85477	Adr85477 Aspergill
C 109	13	59.1	797	3	AAV78471	Aav78471 Plant SDF	C 182	13	59.1	2933	5	AAH89905	Aah89905 Human bon
110	13	59.1	816	2	AAK30465	Aak30465 H. pylori	C 183	13	59.1	2991	4	ABK43659	Abk43659 DNA encod
111	13	59.1	816	2	AAK30429	Aak30429 H. pylori	C 184	13	59.1	2991	12	ADL54046	Adl54046 cDNA enco
112	13	59.1	816	4	AAS53726	Aas53726 Helicobac	C 185	13	59.1	3085	13	ADR84890	Adr84890 Aspergill
113	13	59.1	816	4	AAS53890	Aas53890 Helicobac	C 186	13	59.1	3170	6	ABZ35234	Abz35234 Human gen
114	13	59.1	816	8	ACA34980	Aca34980 Prokaryot	C 187	13	59.1	3273	10	ADQ79065	Adq79065 Human pro
C 115	13	59.1	833	10	ACC43927	Acc43927 Nucleotid	C 188	13	59.1	3523	6	ABQ54610	Abq54610 Human ova
C 116	13	59.1	840	2	AAT68162	Aat68162 H. pylori	C 189	13	59.1	3849	4	AAI63871	Aai63871 Human pol
C 117	13	59.1	885	5	ABV30274	Abv30274 Human pro	C 190	13	59.1	3849	12	ADM24422	Adm24422 Human PRO
C 118	13	59.1	885	3	AAC77620	Aac77620 Human can	C 191	13	59.1	3854	2	AAT97610	Aat97610 Human E2A
119	13	59.1	944	6	ABK65152	Abk65152 Arabidops	C 192	13	59.1	3854	8	ABT18210	Abt18210 Aspergill
120	13	59.1	947	10	ADQ46634	Adq46634 Thalecres	C 193	13	59.1	3867	8	ABT20024	Abt20024 Aspergill
121	13	59.1	947	10	ADQ30295	Adq30295 Plant yle	C 194	13	59.1	3872	10	ADQ79063	Adq79063 Human pro
122	13	59.1	947	12	ADL41550	Adl41550 Plant tra	C 195	13	59.1	3914	12	AQ86121	Aq86121 Human tum
123	13	59.1	947	12	ADQ001654	Adq001654 Thalecres	C 196	13	59.1	3914	13	ACN38620	Acn38620 Tumour-as
124	13	59.1	954	5	AAH65497	Aah65497 C glutami	C 197	13	59.1	3916	6	ABZ78236	Abz78236 A. niger
125	13	59.1	1024	6	ABX65613	Abx65613 Helicobac	C 198	13	59.1	3919	13	ADT05424	Adt05424 Haemophil
C 126	13	59.1	1026	4	AAI81237	Aai81237 Human pol	C 199	13	59.1	3922	9	ACH03928	Ach03928 Human cdn
C 127	13	59.1	1065	5	AAK70168	Aak70168 DNA encod	C 200	13	59.1	3935	8	ABZ34770	Abz34770 Coding se
128	13	59.1	1137	13	ADS49156	Ads49156 Bacterial	C 201	13	59.1	3935	8	ACC50076	Acc50076 Breast ca
C 129	13	59.1	1140	3	AAC59746	Aac59746 Human sec	C 202	13	59.1	3935	10	ADF90653	Adf90653 Human hep
130	13	59.1	1146	8	ACA44595	Aca44595 Prokaryot	C 203	13	59.1	4025	10	ADQ79067	Adq79067 Human pro
131	13	59.1	1161	10	ADQ30376	Adq30376 Bacterial	C 204	13	59.1	4033	13	ADR85839	Adr85839 Aspergill
132	13	59.1	1387	10	ADQ30625	Adq30625 Plant yle	C 205	13	59.1	4105	8	ABT18193	Abt18193 Aspergill
133	13	59.1	1387	12	ADL41852	Adl41852 Plant tra	C 206	13	59.1	4105	8	ABT20007	Abt20007 Aspergill
134	13	59.1	1387	12	ADQ62988	Adq62988 Transcrip	C 207	13	59.1	4125	13	ADR44022	Adr44022 Human col
135	13	59.1	1411	6	ABN97326	Abn97326 Gene #382	C 208	13	59.1	4657	13	ADR85252	Adr85252 Aspergill
136	13	59.1	1411	13	ADQ86272	Adq86272 Human tum	C 209	13	59.1	4894	6	ABA04591	Abaa04591 MOL3 codi
137	13	59.1	1411	13	ADQ87432	Adq87432 Human tum	C 210	13	59.1	4894	10	ADJ787653	Adj787653 G-coupled
138	13	59.1	1419	12	ADQ95933	Adq95933 T cell ac	C 211	13	59.1	5195	10	ADF59868	Adf59868 Human con
139	13	59.1	1422	12	ADQ95991	Adq95991 T cell ac	C 212	13	59.1	5733	3	AAA95416	Aaa95416 Aspergill
C 140	13	59.1	1476	4	AAI60351	Aai60351 Human pol	C 213	13	59.1	5869	10	ADQ62578	Adq62578 Human gen
C 141	13	59.1	1539	10	ADC21639	Adc21639 Thogoto v	C 214	13	59.1	6373	4	ABLI0476	Abli0476 Drosophil
142	13	59.1	1546	4	AAI58565	Aai58565 Human pol	C 215	13	59.1	6657	13	ADR84665	Adr84665 Aspergill
143	13	59.1	1546	5	ADQ98782	Adq98782 DNA encod	C 216	13	59.1	7581	4	AAF85096	Aaf85096 Nucleotid
144	13	59.1	1546	9	ADB48542	Adb48542 Novel hum	C 217	13	59.1	7811	4	ABLI10750	Abli10750 Drosophil
C 145	13	59.1	1556	4	AAI63946	Aai63946 Human pol	C 218	13	59.1	9085	13	ADR84303	Adr84303 Aspergill
C 146	13	59.1	1556	4	AAK31613	Aak31613 cDNA enco	C 219	13	59.1	10303	4	ABLI13738	Abli13738 Drosophil
C 147	13	59.1	1556	4	ABK43947	Abk43947 DNA encod	C 220	13	59.1	11611	13	ADR03846	Adr03846 Carotenoi
C 148	13	59.1	1556	12	ADL54334	Adl54334 cDNA enco	C 221	13	59.1	11611	13	ADR03926	Adr03926 Genetical
C 149	13	59.1	1556	12	ADM24497	Adm24497 Human PRO	C 222	13	59.1	13160	5	ABA15804	Abai5804 Human ner
C 150	13	59.1	1583	3	AAC40650	Aac40650 Arabidops	C 223	13	59.1	13160	5	ADM20183	Adm20183 Alternati
C 151	13	59.1	1639	8	ADA73069	Ada73069 Rice gene	C 224	13	59.1	13189	5	ABA15805	Abai5805 Human ner
C 152	13	59.1	1683	10	ADQ81196	Adq81196 Orf12 cod	C 225	13	59.1	13189	5	ADM20184	Adm20184 Alternati
153	13	59.1	1739	12	ADL42509	Adl42509 Plant tra	C 226	13	59.1	15739	13	ADR03845	Adr03845 Carotenoi
154	13	59.1	1767	8	ABT21218	Abt21218 Aspergill	C 227	13	59.1	15739	13	ADR03925	Adr03925 Genetical
155	13	59.1	1775	12	ADL42510	Adl42510 plant tra	C 228	13	59.1	16103	13	ADR03904	Adr03904 Carotenoi
C 156	13	59.1	1778	10	ADBS3775	Adbs3775 Primary r	C 229	13	59.1	16103	13	ADR03984	Adr03984 Genetical
C 157	13	59.1	1778	12	ADQ24857	Adq24857 Rat novel	C 230	13	59.1	16161	6	AAD36071	Aad36071 Human adi
158	13	59.1	1791	8	ABT19398	Abt19398 Aspergill	C 231	13	59.1	16245	13	ADR03878	Adr03878 B trispor
C 159	13	59.1	1830	6	ABK94898	Abk94898 Human nov	C 232	13	59.1	16245	13	ADR03958	Adr03958 Genetical
160	13	59.1	1854	8	ABT18804	Abt18804 Aspergill	C 233	13	59.1	16954	13	ADR03886	Adr03886 Carotenoi
161	13	59.1	1867	8	ABT20620	Abt20620 Aspergill	C 234	13	59.1	16954	13	ADR03885	Adr03885 Carotenoi
162	13	59.1	2000	8	ADA73355	Ada73355 Rice Gene	C 235	13	59.1	16954	13	ADR03965	Adr03965 Genetical
163	13	59.1	2025	8	ABT19381	Abt19381 Aspergill	C 236	13	59.1	16954	13	ADR03966	Adr03966 Genetical
164	13	59.1	2035	8	ABT21201	Abt21201 Aspergill	C 237	13	59.1	17118	13	ADR03890	Adr03890 Carotenoi
C 165	13	59.1	2047	6	ABL99809	Abi99809 Human sec	C 238	13	59.1	17118	13	ADR03970	Adr03970 Genetical
C 166	13	59.1	2047	8	ABX62972	Abx62972 Human act	C 239	13	59.1	17238	13	ADR03881	Adr03881 Carotenoi

240	13	59.1	17238	13	AD03880	Ad03880 Carotenoi	XX	SARS coronavirus nucleotide sequence.
241	13	59.1	17238	13	AD03961	Ad03961 Genetical	DE	
242	13	59.1	17238	13	AD03960	Ad03960 Genetical	XX	
243	13	59.1	17593	13	AD03884	Ad03884 Carotenoi	KW	small interfering RNA; siRNA; modified ribonucleotide;
244	13	59.1	17593	13	AD03964	Ad03964 Genetical	KW	viral replication inhibition; hepatitis C virus; HCV; hepatitis C;
245	13	59.1	17756	13	AD03889	Ad03889 Carotenoi	KW	antiinflammatory; hepatotropic; virucide; hepatitis A virus;
246	13	59.1	17756	13	AD03969	Ad03969 Genetical	KW	hepatitis D virus; hepatitis E virus; Ebola virus; influenza virus;
247	13	59.1	17877	13	AD03879	Ad03879 Carotenoi	KW	rotavirus; reovirus; retrovirus; poliovirus; human papilloma virus;
248	13	59.1	17877	13	AD03959	Ad03959 Genetical	KW	metapneumoniavirus; coronavirus; viral infection; gene; ds.
249	13	59.1	18333	13	AD03893	Ad03893 Carotenoi	XX	
250	13	59.1	18333	13	AD03973	Ad03973 Genetical	OS	SARS coronavirus.
251	13	59.1	18449	13	AD03882	Ad03882 Carotenoi	XX	
252	13	59.1	18449	13	AD03891	Ad03891 Carotenoi	PN	WO2004011647-A1.
253	13	59.1	18449	13	AD03883	Ad03883 Carotenoi	XX	
254	13	59.1	18449	13	AD03962	Ad03962 Genetical	PD	05-FEB-2004.
255	13	59.1	18449	13	AD03963	Ad03963 Genetical	XX	
256	13	59.1	18449	13	AD03971	Ad03971 Genetical	PF	25-JUL-2003; 2003WO-US023104.
257	13	59.1	18617	13	AD03892	Ad03892 Carotenoi	XX	
258	13	59.1	18617	13	AD03972	Ad03972 Genetical	PR	26-JUL-2002; 2002US-0398605P.
259	13	59.1	19491	13	AD03887	Ad03887 Carotenoi	XX	(CHIR) CHIRON CORP.
260	13	59.1	19491	13	AD03967	Ad03967 Genetical	PA	Han J, Seo MY, Houghton M;
261	13	59.1	21300	13	AD03888	Ad03888 Carotenoi	XX	WPI; 2004-143862/14.
262	13	59.1	21300	13	AD03968	Ad03968 Genetical	PI	New RNase resistant small interfering RNA, useful for treating viral
263	13	59.1	23118	4	AAK71708	AAK71708 Human imm	XX	infections, e.g., hepatitis C, influenza virus or coronavirus infection.
264	13	59.1	23171	11	ACN44326	ACN44326 Human gen	DR	Example 10; Fig 3; 74pp; English.
265	13	59.1	27571	12	ADQ59500	ADQ59500 Human can	XX	
c 266	13	59.1	29598	2	AAV49654	AAV49654 Human SC2	PT	
267	13	59.1	33249	4	ABL15430	ABL15430 Drosophil	PT	
c 268	13	59.1	52312	13	ABD33555	ABD33555 Murine ca	XX	
269	13	59.1	59767	13	ABD32905	ABD32905 Mouse can	PS	
270	13	59.1	68750	3	AZ55887	AZ55887 Soranglum	XX	
c 271	13	59.1	72149	10	ADBE81173	ADBE81173 ML-236B s	CC	The present invention describes a small interfering RNA (siRNA) which
272	13	59.1	85814	13	ADT05644	ADT05644 Haemophil	CC	comprises a modified ribonucleotide, where the siRNA is resistant to
273	13	59.1	91823	10	ADL13497	ADL13497 Osteoarth	CC	RNase and retains the ability to inhibit viral replication. Also
274	13	59.1	94618	3	AAF22285	AAF22285 BAC conta	CC	described: (1) inactivating a virus in a patient; (2) making a modified
c 275	13	59.1	96593	9	ADA02600	ADA02600 Human RUN	CC	siRNA that targets a nucleic acid sequence in a virus; (3) a double-
c 276	13	59.1	96593	10	ADB72338	ADB72338 Human RUN	CC	stranded RNA molecule of 10-30 nucleotides that inhibits replication of
c 277	13	59.1	96593	10	ADE95848	ADE95848 Human RUN	CC	hepatitis C virus (HCV); (4) inducing targeted RNA interference toward
c 278	13	59.1	96599	9	ADA02981	ADA02981 Mouse Map	CC	HCV in hepatic cells; (5) inhibiting replication of HCV; (6) a vector
c 279	13	59.1	96599	10	ADB72719	ADB72719 Mouse Map	CC	comprising a DNA segment encoding the RNA molecule; (7) a host cell
c 280	13	59.1	96599	10	ADC85461	ADC85461 Mouse Map	CC	comprising the vector of (6); (8) inhibiting replication of HCV in cells
c 281	13	59.1	96599	12	ADM74576	ADM74576 Murine ca	CC	carrying HCV; (9) treating hepatitis C in a subject; (10) a modified
c 282	13	59.1	110000	2	AT42063_05	Continuation (6 of	CC	siRNA molecule comprising a double-stranded RNA molecule of 10-30
c 283	13	59.1	110000	11	ACN43998_2	Continuation (3 of	CC	nucleotides in length, which mediates RNA interference toward a target
c 284	13	59.1	17424	6	ABL68122	ABL68122 Ovary can	CC	agent or virus and is linked to at least one receptor-binding ligand; and
c 285	13	59.1	177380	8	ACF62751	ACF62751 Cancer ba	CC	(11) inducing targeted RNA interference in a patient. The modified siRNA
c 286	13	59.1	177380	8	ADB20870	ADB20870 MRPl base	CC	molecules have antiinflammatory, hepatotropic and virucide activities.
c 287	13	59.1	177380	10	ADB87959	ADB87959 Human UGT	CC	The modified RNA molecules are useful for inactivating virus in mammalian
c 288	13	59.1	177380	10	ADB96942	ADB96942 Human MDR	CC	cells. The siRNAs are useful for treating hepatitis C virus, hepatitis A
c 289	13	59.1	177380	10	ADB92133	ADB92133 Human MDR	CC	virus, hepatitis D virus, hepatitis E virus, Ebola virus, influenza
c 290	13	59.1	181343	12	ADQ19573	ADQ19573 Human sof	CC	virus, rotavirus, reovirus, retrovirus, poliovirus, human papilloma
c 291	13	59.1	199868	12	ADQ97831	ADQ97831 Mouse can	CC	virus, metapneumoniavirus or coronavirus infections. The methods of the
c 292	13	59.1	203654	10	ABX16034	ABX16034 Human gen	CC	invention can be used to correct or compensate for cellular physiological
c 293	13	59.1	209484	11	ACN44126	ACN44126 Human gen	CC	abnormalities involved in conferring susceptibility to viral infections
c 294	13	59.1	220224	11	ACN44702	ACN44702 Human gen	CC	in patients and/or alleviate symptoms of a viral infection in patients.
c 295	13	59.1	260803	13	ABD32730	ABD32730 Human can	CC	The present sequence represents the SARS coronavirus nucleotide sequence,
c 296	13	59.1	349980	5	AAH68525	AAH68525 C glutami	CC	which is used in an example from the present invention.
c 297	13	54.5	25	9	ACK27897	ACK27897 Human mic	XX	
c 298	13	54.5	25	9	ACI79106	ACI79106 Human mic	XX	
c 299	13	54.5	25	9	ACI12036	ACI12036 Human mic	XX	
c 300	12	54.5	27	2	AAH80816	AAH80816 A.Chalian	SQ	Sequence 29751 BP; 8478 A; 5941 C; 6188 G; 9144 T; 0 U; 0 Other;

Query Match 90.9%; Score 20; DB 12; Length 29751;

Best Local Similarity 75.0%; Pred. No. 0.033;

Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 GUGAACUCACUCGUGAGCUC 20

Dd |:|:|:|:|:|:|:|:|:|:|

776 GTGAACCTCACTCGTGAGCTC 795

RESULT 2

ID ADJ39000

AC ADJ39000;

XX DT 06-MAY-2004 (first entry)

ALIGNMENTS

RESULT 1

ADJ39000

ID ADJ39000 standard; DNA; 29751 BP.

XX

AC ADJ39000;

XX

DT 06-MAY-2004 (first entry)


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OS Unidentified.
PN WO2003020025-A2.
XX
XX
PD 13-MAR-2003.
XX
XX 30-AUG-2002; 2002WO-US027882.
XX
XX 31-AUG-2001; 2001US-0316319P.
XX
XX (DOWC ) DOW CHEM CO.
XX
XX Shukla V, Meade T, Larrinua I;
XX WPI; 2003-290133/28.
XX
XX New isolated nucleic acid having expression that results in an insect
PT resistant phenotype, useful for conferring insect resistance and for
PT producing insect-resistant plants.
XX
XX Claim 1; SEQ ID NO 856; 396pp; English.
XX
XX This invention relates to a novel isolated nucleic acid comprising, or
CC hybridising under low stringent conditions to, any of the 1214 nucleic
CC acid sequences given in the specification, where the expression of the
CC nucleic acid in a plant results in an insect resistant phenotype. The
CC invention may be useful as a plant protectant or for gene therapy. The
CC genes are derived from Arabidopsis thaliana, Nicotiana benthamiana, Oryza
CC sativa and Papaver rhoeas. The isolated nucleic acid and vector are
CC useful for conferring insect resistance and for producing insect-
CC resistant plants. The present sequence is that of a DNA sequence of the
CC invention which may confer insect resistance to plants.
XX
XX Sequence 619 BP; 133 A; 183 C; 177 G; 126 T; 0 U; 0 Other;
XX
XX Query Match 72.7%; Score 16; DB 11; Length 619;
XX Best Local Similarity 75.0%; Pred. No. 7.4;
XX Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
XX
XX 6 CUCACUCGUGAGCUCT 21
XX 599 CTCACCTCGTGAGCTCT 614
XX
XX RESULT 5
XX ADM44886
XX ID ADM44886 standard; DNA; 672 BP.
XX
XX AC ADM44886;
XX
XX DT 03-JUN-2004 (first entry)
XX
XX Insect resistance associated DNA sequence SeqID293.
XX
XX insect resistant phenotype; plant protectant; gene therapy;
XX Arabidopsis thaliana; Nicotiana benthamiana; Oryza sativa;
XX Papaver rhoeas; rice; insect resistance; insect-resistant plant; ds.
XX
XX Unidentified.
XX
XX WO2003020025-A2.
XX
XX 13-MAR-2003.
XX
XX 30-AUG-2002; 2002WO-US027882.
XX
XX 31-AUG-2001; 2001US-0316319P.
XX
XX (DOWC ) DOW CHEM CO.
XX
XX Shukla V, Meade T, Larrinua I;
XX WPI; 2003-290133/28.
XX
XX The invention comprises DNA sequences which confer an altered metabolic

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XX New isolated nucleic acid having expression that results in an insect
PT resistant phenotype, useful for conferring insect resistance and for
PT producing insect-resistant plants.
XX
XX Claim 1; SEQ ID NO 293; 396pp; English.
XX
XX This invention relates to a novel isolated nucleic acid comprising, or
CC hybridising under low stringent conditions to, any of the 1214 nucleic
CC acid sequences given in the specification, where the expression of the
CC nucleic acid in a plant results in an insect resistant phenotype. The
CC invention may be useful as a plant protectant or for gene therapy. The
CC genes are derived from Arabidopsis thaliana, Nicotiana benthamiana, Oryza
CC sativa and Papaver rhoeas. The isolated nucleic acid and vector are
CC useful for conferring insect resistance and for producing insect-
CC resistant plants. The present sequence is that of a DNA sequence of the
CC invention which may confer insect resistance to plants.
XX
XX Sequence 672 BP; 144 A; 197 C; 192 G; 139 T; 0 U; 0 Other;
XX
XX Query Match 72.7%; Score 16; DB 11; Length 672;
XX Best Local Similarity 75.0%; Pred. No. 7.4;
XX Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
XX
XX 6 CUCACUCGUGAGCUCT 21
XX 619 CTCACCTCGTGAGCTCT 634
XX
XX RESULT 6
XX ADK57646
XX ID ADK57646 standard; DNA; 686 BP.
XX
XX AC ADK57646;
XX
XX DT 06-MAY-2004 (first entry)
XX
XX Plant DNA sequence which confers altered metabolic characteristic #5029.
XX
XX altered metabolic characteristic; plant; acid metabolism;
XX alcohol metabolism; fatty acid metabolism;
XX branched fatty acid metabolism; alkaloid metabolism;
XX amino acid metabolism; ester metabolism; glyceride metabolism;
XX phenolic metabolism; carbohydrate metabolism; sterol metabolism;
XX terpene metabolism; isoprenoid metabolism; alkene metabolism;
XX alkyne metabolism; hydrocarbon metabolism; ketone metabolism;
XX quinone metabolism; disease resistance; gene shuffling; sexual PCR; ds.
XX
XX Unidentified.
XX
XX WO2003020936-A1.
XX
XX 13-MAR-2003.
XX
XX 30-AUG-2002; 2002WO-US027884.
XX
XX 31-AUG-2001; 2001US-0316471P.
XX
XX (DOWC ) DOW CHEM CO.
XX
XX (DOWC ) DOW AGROSCIENCES LLC.
XX
XX Weglarz T, Gachotte D, Blakeslee B, McCreary DA, Pell RJ;
XX Oriedo JVB, Crosley R, Reddy AS, Shukla V, Larrinua I, Miller BA;
XX WPI; 2003-313091/30.
XX
XX Novel genes that confer altered metabolic characteristics in Nicotiana
PT benthamiana plants, useful for altering the levels of metabolites e.g.
PT acids, fatty acids, amino acids, carbohydrates, hydrocarbons and sterols.
XX
XX Claim 1; SEQ ID NO 5029; 2576pp; English.
XX
XX The invention comprises DNA sequences which confer an altered metabolic

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characteristic when they are expressed in a plant. The DNA sequences of the invention are useful for producing plants with an altered metabolic characteristic, such as: altered acid metabolism, alcohol metabolism, fatty acid metabolism, branched fatty acid metabolism, alkaloid or other base metabolism, altered amino acid metabolism, altered ester metabolism, altered glyceride metabolism, altered phenolic metabolism, altered carbohydrate metabolism, altered sterol, oxygenated terpene, or isoprenoid metabolism, alkene or alkyne metabolism, hydrocarbon metabolism, ketone or quinone metabolism. The DNA sequences of the invention may be used to provide disease resistance in a plant and gene shuffling or sexual PCR procedures. The present nucleic acid represents a DNA sequence of the invention.

Query Match	72.7%	Score 16;	DB 10;	Length 686;
Best Local Similarity	75.0%	Pred. No. 7.4;		
Matches 12;	Conservative	4;	Mismatches	0;
Indels	0;	Gaps	0;	

Qy 6 CUCACUCGUGAGCUCT 21
|:|:|:|:|:|:|:|:|:|:
Db 620 CTCACCTCGTGAGCTCT 635

RESULT 7
ADK54332
ID ADK54332 standard; DNA; 686 BP.
XX
XX ADK54332;
XX
XX
XX
XX 06-MAY-2004 (first entry)
XX
DE Plant DNA sequence which confers altered metabolic characteristic #1715.

CC altered glyceride metabolism, altered phenolic metabolism, altered
CC carbohydrate metabolism, altered sterol, oxygenated terpene, or
CC isoprenoid metabolism, alkene or alkyne metabolism, hydrocarbon
CC metabolism, ketone or quinone metabolism. The DNA sequences of the
CC invention may be used to provide disease resistance in a plant and gene
CC shuffling or sexual PCR procedures. The present nucleic acid represents a
CC DNA sequence of the invention.

Query Match 72.7%; Score 16; DB 10; Length 686;
Best Local Similarity 75.0%; Pred. No. 7.4;
Matches 12; Conservative 4; Mismatches 0; Indels

Qy 6 CUCACUCGUGAGCTCT 21
|:|:|:|:|:|:|:
Db 620 CTCACCTCGTGAGCTCT 635

RESULT 8	
ADM45452	
ID	ADM45452 standard; DNA; 696 BP.
XX	
XX	
AC	ADM45452;
XX	
DT	03-JUN-2004 (first entry)
XX	
DE	Insect resistance associated DNA sequence SegID859.
XX	
DE	
KW	insect resistant phenotype; plant protectant; gene therapy;
KW	Arabidopsis thaliana; Nicotiana glauca; Oryza sativa;
KW	Papaver rhoeas; rice; insect resistance; insect-resistant plant; ds.
XX	
OS	Unidentified.

branched fatty acid metabolism; alkaloid metabolism;
amino acid metabolism; ester metabolism; glyceride metabolism;
phenolic metabolism; carbohydrate metabolism; sterol metabolism;
terpene metabolism; isoprenoid metabolism; alkene metabolism;
alkyne metabolism; hydrocarbon metabolism; ketone metabolism;
quinone metabolism; disease resistance; gene shuffling; sexual
PCR; ds.

XX (DOWC) DOW CHEM CO.
PA
XX
PI Shukla V. Meade T. Larrinua

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Db      622 CTCACCTCGTGAGCTCT 637
      ||:||||:||||:||||:||||:
RESULT 9
ABN69216
ID ABN69216 standard; DNA; 534 BP.
XX AC ABN69216;
XX DT 01-JUL-2002 (first entry)
XX DE Streptococcus polynucleotide SEQ ID NO 6345.
XX KW Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;
XX KW group A streptococcus; Streptococcus pyogenes; antibacterial; gene;
XX KW antiinflammatory; infection; vaccine; meningitis; gene therapy; ds.
XX OS Streptococcus pyogenes.
XX PN WO200234771-A2.
XX PD 02-MAY-2002.
XX PF 29-OCT-2001; 2001WO-GB004789.
XX PR 27-OCT-2000; 2000GB-00026333.
XX PR 24-NOV-2000; 2000GB-00028727.
XX PR 07-MAR-2001; 2001GB-00005640.
XX PA (CHIR-) CHIRON SPA.
XX PA (GENO-) INST GENOMIC RES.
XX PI Telford J, Masignani V, Margarit Y Rosi, Grandi G, Fraser C;
XX PI Tettelin H;
XX DR WPI; 2002-352536/38.
XX DR P-PSDB; ABP28585.
XX PT New Streptococcus protein for the treatment or prevention of infection or
XX PT disease caused by Streptococcus bacteria, such as meningitis, and for
XX PT detecting a compound that binds to the protein.
XX PS Claim 7; Page 3799; 4525pp; English.
XX CC The invention relates to a protein (ABP25413-ABP30895) from group B
XX CC streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS
XX CC (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in
XX CC the specification. The proteins have antibacterial and antiinflammatory
XX CC activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and
XX CC antibodies that bind (I) are used in the manufacture of medicaments for
XX CC the treatment or prevention of infection or disease caused by
XX CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.
XX CC Nucleic acids encoding (I) are used to detect Streptococcus in a
XX CC biological sample. (I) is used to determine whether a compound binds to
XX CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be
XX CC used as a vaccine or diagnostic composition. The disease caused by
XX CC Streptococcus that is prevented or treated may be meningitis. Nucleic
XX CC acid encoding (I) may be used to recombinantly produce (I) and may be
XX CC used in gene therapy. Antibodies to (I) are used for affinity
XX CC chromatography, immunoassays, and distinguishing/identifying
XX CC Streptococcus proteins
XX SQ Sequence 534 BP; 186 A; 101 C; 109 G; 138 T; 0 U; 0 Other;
Query March 68.2%; Score 15; DB 6; Length 534;
Best Local Similarity 80.0%; Pred. No. 29;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
Oy 3 GAACUCACUCGUGAG 17
      |||:||||:||||:
Db 94 GAACCTACTCTGTGAG 108

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RESULT 10
ACA50276
ID ACA50276 standard; DNA; 537 BP.
XX AC ACA50276;
XX DT 19-JUN-2003 (first entry)
XX DE Prokaryotic essential gene #31933.
XX KW Antisense; ds; prokaryotic essential gene; cell proliferation;
XX KW drug design; gene.
XX OS Streptococcus pyogenes.
XX PN WO200277183-A2.
XX PD 03-OCT-2002.
XX PF 21-MAR-2002; 2002WO-US009107.
XX PR 06-SEP-2001; 2001US-00815242.
XX PR 25-OCT-2001; 2001US-00948993.
XX PR 08-FEB-2002; 2002US-00072851.
XX PR 06-MAR-2002; 2002US-0362699P.
XX PA (ELIT-) ELITRA PHARM INC.
XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
XX PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX DR WPI; 2003-029926/02.
XX DR P-PSDB; ABU46406.
XX PT New antisense nucleic acids, useful for identifying proteins or screening
XX PT for homologous nucleic acids required for cellular proliferation to
XX PT isolate candidate molecules for rational drug discovery programs.
XX PS Claim 14; SEQ ID NO 38146; 1766pp; English.
XX CC The invention relates to an isolated nucleic acid comprising any one of
XX CC the 6213 antisense sequences given in the specification where expression
XX CC of the nucleic acid inhibits proliferation of a cell. Also included are:
XX CC (1) a vector comprising a promoter operably linked to the nucleic acid
XX CC encoding a polypeptide whose expression is inhibited by the antisense
XX CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
XX CC polypeptide or its fragment whose expression is inhibited by the
XX CC antisense nucleic acid; (4) an antibody capable of specifically binding
XX CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
XX CC proliferation or the activity of a gene in an operon required for
XX CC proliferation; (7) identifying a compound that influences the activity of
XX CC the gene product or that has an activity against a biological pathway
XX CC required for proliferation, or that inhibits cellular proliferation; (8)
XX CC identifying a gene required for cellular proliferation or the biological
XX CC pathway in which a proliferation-required gene or its gene product lies
XX CC or a gene on which the test compound that inhibits proliferation of an
XX CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
XX CC compound's activity; (11) a culture comprising strains in which the gene
XX CC product is overexpressed or underexpressed; (12) determining the extent
XX CC to which each of the strains is present in a culture or collection of
XX CC strains; or (13) identifying the target of a compound that inhibits the
XX CC proliferation of an organism. The antisense nucleic acids are useful for
XX CC identifying proteins or screening for homologous nucleic acids required
XX CC for cellular proliferation to isolate candidate molecules for rational
XX CC drug discovery programs, or for screening homologous nucleic acids
XX CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
XX CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is one of the target
XX CC prokaryotic essential genes. Note: The sequence data for this patent did
XX CC not form part of the printed specification, but was obtained in
XX CC electronic format directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences

```
XX SQ Sequence 537 BP; 188 A; 101 C; 109 G; 139 T; 0 U; 0 Other;
Query Match 68.2%; Score 15; DB 8; Length 537;
Best Local Similarity 80.0%; Pred. No. 29;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 GAACUCACUCUGAG 17
    ||||:||||:||||
Db 94 GAACCTCACTCGTGAG 108

RESULT 11
ABS61473/c
ID ABS61473 standard; cDNA; 627 BP.
XX AC ABS61473;
XX XX
XX 05-NOV-2002 (first entry)
XX DE Prostate specific nucleic acid DEX0259_81.
XX KW Human; ss; prostate specific nucleic acid; PSNA; prostate cancer;
XX KW cytostatic; non-cancerous prostate disease; PSP; vaccine;
XX KW prostate specific protein; metastasis.
XX OS Homo sapiens.
XX PN WO200242776-A2.
XX PD 30-MAY-2002.
XX XX
XX 01-NOV-2001; 2001WO-US045654.
XX PR 01-NOV-2000; 2000US-0244782P.
XX XX
XX (DIAD-) DIADEXUS INC.
XX PA Sun Y, Recipon H, Chen S, Liu C;
XX PI WPI; 2002-490217/52.
XX DR
XX New polypeptide useful for diagnosing and monitoring the presence and
XX PT metastases of prostate cancer in a patient and as a component in
XX PT databases for search analysis as well as in sequence analysis algorithms.
XX PS Claim 1; Page 183-184; 242pp; English.
XX CC
XX The invention relates to an isolated polypeptide comprising a sequence
XX CC with 60 % identity to one of prostate specific protein (PSP) sequences,
XX CC or comprising an amino acid sequence encoded by one of 136 nucleotide
XX CC prostate specific nucleic acid sequences, PSNA, (or a sequence that
XX CC hybridises to it or is 60% identical to it), given in the specification.
XX CC Also included are a vector comprising the polynucleotide, a host cell
XX CC comprising the vector, an antibody specific for the PSP proteins and a
XX CC vaccine comprising the protein or polynucleotide. The PSP and PSNA are
XX CC useful for diagnosing and monitoring the presence and metastases of
XX CC prostate cancer in a patient. The PSNA is useful for determining the
XX CC level PSNA in a sample. An antibody to the PSP is useful for determining
XX CC the presence of prostate specific protein in a sample, and for treating a
XX CC patient with prostate cancer, which induces an immune response against
XX CC the prostate cancer cell expressing the nucleic acid or polypeptide and a
XX CC kit is useful for detecting a risk of cancer or presence of cancer in a
XX CC patient. PSNA is useful as hybridisation probes to detect, characterise
XX CC and quantify hybridising nucleic acids from both genomic and transcript-
XX CC derived nucleic acid samples and also in microarrays. Sequences of PSP
XX CC and PSNA are useful as components in databases for search analysis as
XX CC well as in sequence analysis algorithms. PSNA is useful to drive in vivo
XX CC expression of PSP. The present sequence is a PSNA of the invention
XX SQ Sequence 627 BP; 129 A; 152 C; 169 G; 177 T; 0 U; 0 Other;
Query Match 68.2%; Score 15; DB 6; Length 627;

Best Local Similarity 80.0%; Pred. No. 29;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 GAACUCACUCUGAG 17
    ||||:||||:||||
Db 224 GAACCTCACTCGTGAG 210

RESULT 12
ADR61500
ID ADR61500 standard; cDNA; 1101 BP.
XX AC ADR61500;
XX XX
XX 02-DEC-2004 (first entry)
XX DE Cotton cDNA sequence, SEQ ID 2281.
XX KW Cotton; ss; plant; cold tolerance; growth rate; cell cycle pathway;
XX KW drought tolerance; plant disease resistance; galactomannan; lignin;
XX KW plant growth regulator; heat tolerance; herbicide tolerance;
XX KW homologous recombination; extreme osmotic condition tolerance;
XX KW pathogen resistance; pest resistance; yield; photosynthesis; seed oil;
XX KW stress resistance.
XX OS Gossypium hirsutum.
XX PN US2004181830-A1.
XX PD 16-SEP-2004.
XX XX
XX 29-JAN-2004; 2004US-00767795.
XX XX
XX 07-MAY-2001; 2001US-00849529.
XX PR 12-DEC-2001; 2001US-00021323.
XX XX
XX (KOVA/) KOVALIC D K.
XX PA (ZHOU/) ZHOU Y.
XX PA (CAOY/) CAO Y.
XX XX
XX Kovalic DK, Zhou Y, Cao Y;
XX PI WPI; 2004-667718/65.
XX DR
XX New recombinant nucleic acid molecules and polypeptides from Gossypium
XX PT hirsutum, useful for producing plants with improved biological
XX PT characteristics (e.g. improved plant cold or drought tolerance).
XX PS Claim 1; SEQ ID NO 2281; 14pp; English.
XX CC
XX The invention relates to a recombinant polynucleotide comprising any of
XX CC the 58798 Cotton plant cDNA sequences mentioned in the specification.
XX CC Also a recombinant polypeptide comprising any of the 58798 amino acid
XX CC sequences mentioned in the specification and producing a plant having an
XX CC improved property. Producing a plant having an improved property
XX CC comprises transforming a plant with a recombinant construct comprising a
XX CC promoter region functional in a plant cell operably joined to a
XX CC polynucleotide comprising a coding sequence for a polypeptide associated
XX CC with the property, and growing the transformed plant. The polypeptide is
XX CC useful for improving plant cold tolerance, manipulating growth rate in
XX CC plant cells by modification of the cell cycle pathway, improving plant
XX CC drought tolerance, providing increased resistance to plant disease,
XX CC producing galactomannan (or lignin or plant growth regulators), improving
XX CC plant heat tolerance, improving plant tolerance to herbicides, increasing
XX CC the rate of homologous recombination in plants, improving plant tolerance
XX CC to extreme osmotic conditions or to pathogens or pests, improving yield
XX CC by modification of photosynthesis, modifying seed oil or protein yield
XX CC and/or content, improving yield by modification of carbohydrate, nitrogen
XX CC or phosphorus use and/or uptake, or improving yield by providing improved
XX CC plant growth and development under at least one stress condition. The
XX CC polynucleotide and polypeptide may also be used in recombinant DNA
XX CC constructs, in physical arrays of molecules, as plant breeding markers,
XX CC or in computer-based storage and analysis systems. The present sequence
```


CC is a Cotton plant cDNA of the invention. NOTE: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=20040181830. However only 6585
CC polynucleotide sequences were available, the remaining 52213
CC polynucleotides and all 58798 protein sequences were not present.

XX SQ Sequence 1101 BP; 308 A; 201 C; 254 G; 338 T; 0 U; 0 Other;

Query Match 68.2%; Score 15; DB 13; Length 1101;
Best Local Similarity 73.3%; Pred. No. 29;
Matches 11; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CUCACUCUGAGTUC 20

Db 1027 CTCACCTCGTGCCTC 1041

RESULT 13

ABAI4473
ID ABA14473 standard; DNA; 1191 BP.

XX AC ABA14473;

DT 23-JAN-2002 (first entry)

XX DE Human nervous system related polynucleotide SEQ ID NO 6804.

XX KW Human; nontropic; neuroprotective; cytostatic; dermatological; virucide;
KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnery;
KW antiparkinsonian; antickling; antianaemic; antiarthritic; cancer;
KW antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
KW antiallergic; antidiabetic; antilucer; anticonvulsant; antifungal;
KW antiparasitic; cardiant; immune disorder; cardiovascular disorder;
KW neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.

XX OS Homo sapiens.

XX PN WO200159063-A2.

XX PD 16-AUG-2001.

XX PF 17-JAN-2001; 2001WO-US001334.

XX PR 31-JAN-2000; 2000US-0179065P.

XX PR 04-FEB-2000; 2000US-0180628P.

XX PR 24-FEB-2000; 2000US-0184664P.

XX PR 02-MAR-2000; 2000US-0186350P.

XX PR 16-MAR-2000; 2000US-0189874P.

XX PR 17-MAR-2000; 2000US-0190076P.

XX PR 18-APR-2000; 2000US-0198123P.

XX PR 19-MAY-2000; 2000US-0205515P.

XX PR 07-JUN-2000; 2000US-0209467P.

XX PR 28-JUN-2000; 2000US-0214886P.

XX PR 30-JUN-2000; 2000US-0215135P.

XX PR 07-JUL-2000; 2000US-0216647P.

XX PR 07-JUL-2000; 2000US-0216880P.

XX PR 11-JUL-2000; 2000US-0217487P.

XX PR 11-JUL-2000; 2000US-0217496P.

XX PR 14-JUL-2000; 2000US-0218290P.

XX PR 26-JUL-2000; 2000US-0220963P.

XX PR 26-JUL-2000; 2000US-0220964P.

XX PR 14-AUG-2000; 2000US-0224518P.

XX PR 14-AUG-2000; 2000US-0224519P.

XX PR 14-AUG-2000; 2000US-0225213P.

XX PR 14-AUG-2000; 2000US-0225214P.

XX PR 14-AUG-2000; 2000US-0225266P.

XX PR 14-AUG-2000; 2000US-0225267P.

XX PR 14-AUG-2000; 2000US-0225268P.

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XX PR 14-AUG-2000; 2000US-0225758P.

XX PR 14-AUG-2000; 2000US-0225759P.

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PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.


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PR 25-SEP-2000; 2000US-0234998P.
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PR 29-SEP-2000; 2000US-0236369P.
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PR 08-NOV-2000; 2000US-0246477P.
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PR 08-NOV-2000; 2000US-0246613P.
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PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
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PR 17-NOV-2000; 2000US-0249244P.

PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250391P.
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PR 05-DEC-2000; 2000US-0251030P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
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PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-541565/60.
XX
XX Nucleic acids encoding 3224 human nervous system antigen polypeptides,
XX useful for preventing, diagnosing and/or treating nervous system cancers
XX and metastases.
XX
XX Disclosure; SEQ ID NO 6803; 1701pp + Sequence Listing; English.
XX
XX The invention relates to novel genes (ABAI1004-ABAI21534) and proteins
XX (ABAI4678-ABAI18001) useful for preventing, treating or ameliorating
XX medical conditions e.g. by protein or gene therapy. The genes are
XX isolated from a range of human tissues disclosed in the specification.
XX The nucleic acids, proteins, antibodies and (ant)agonists are useful in
XX the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
XX ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,
XX breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune
XX disorders e.g. Addison's disease, allergies, autoimmune haemolytic
XX anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
XX multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
XX cardiovascular disorders such as myocardial ischaemias; (d) wound healing
XX ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
XX infectious diseases such as viral, bacterial, fungal and parasitic
XX infections. Note: The sequence data for this patent did not form part of
XX the printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 1191 BP; 335 A; 265 C; 279 G; 312 T; 0 U; 0 Other;
XX
XX Query Match 68.2%; Score 15; DB 5; Length 1191;
XX Best Local Similarity 80.0%; Pred. No. 29;
XX Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 8 CACUCGUGAGCUCTT 22
XX
XX Db 756 CACTCGTGAGCTCTT 770
XX
XX
XX RESULT 15
XX AAI22168/c
XX ID AAI22168 standard; DNA; 1820 BP.
XX
XX AC AAI22168;
XX
XX DT 12-OCT-2001 (first entry)
XX
XX DE Probe #12101 for gene expression analysis in human cervical cell sample.
XX
XX KW Probe; human; microarray; gene expression; cervical epithelial cell;
XX cervical cancer; ss.
```

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XX OS Homo sapiens.
XX PN WO200157278-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US000670.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX PFPI; 2001-488901/53.
XX PT Human genome-derived single exon nucleic acid probes useful for analyzing
XX PT gene expression in human cervical epithelial cells.
XX PS Claim 25; SEQ ID NO 12101; 487pp; English.
XX CC The present invention relates to human single exon nucleic acid probes
XX CC (SENPs). The present sequence is one such probe. The SENPs are derived
XX CC from human HeLa cells. The SENPs can be used to produce a single exon
XX CC microarray, which can be used for measuring human gene expression in a
XX CC sample derived from human cervical epithelial cells. By measuring gene
XX CC expression, the probes are therefore useful in grading and/or staging of
XX CC diseases of the cervix, notably cervical cancer. Note: The sequence data
XX CC for this patent did not form part of the printed specification, but was
XX CC obtained in electronic format directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 1820 BP; 546 A; 406 C; 445 G; 423 T; 0 U; 0 Other;

Query Match 68.2%; Score 15; DB 4; Length 1820;
Best Local Similarity 80.0%; Pred. No. 30;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 8 CACUCGUGAGCUCTT 22
DB 1774 CACTCGTGAGCTCTT 1760

RESULT 16
ABA67247/c
ID ABA67247 standard; DNA; 1820 BP.
XX AC ABA67247;
XX DT 01-FEB-2002 (first entry)
XX DE Human foetal liver single exon nucleic acid probe #15552.
XX KW Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
XX OS Homo sapiens.
XX PN WO200157277-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US000669.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.

XX OS Homo sapiens.
XX PN WO200157277-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US000669.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
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PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX PFPI; 2001-483447/52.
XX PT Human genome-derived single exon nucleic acid probes useful for analyzing
XX PT gene expression in human fetal liver.
XX PS Claim 4; SEQ ID NO 15552; 639pp + Sequence Listing; English.
XX CC The invention relates to a single exon nucleic acid probe for measuring
XX CC human gene expression in a sample derived from human foetal liver. The
XX CC single exon nucleic acid probes may be used for predicting, measuring and
XX CC displaying gene expression in samples derived from human fetal liver. The
XX CC present sequence is a single exon nucleic acid probe of the invention.
XX CC Note: The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 1820 BP; 546 A; 406 C; 445 G; 423 T; 0 U; 0 Other;

Query Match 68.2%; Score 15; DB 4; Length 1820;
Best Local Similarity 80.0%; Pred. No. 30;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 8 CACUCGUGAGCUCTT 22
DB 1774 CACTCGTGAGCTCTT 1760

RESULT 17
AAI47467/c
ID AAI47467 standard; DNA; 1820 BP.
XX AC AAI47467;
XX DT 17-OCT-2001 (first entry)
XX DE Probe #16153 used to measure gene expression in human placenta sample.
XX KW Probe; microarray; human; placenta; antenatal diagnosis;
XX KW genetic disorder; ss.
XX OS Homo sapiens.
XX PN WO200157272-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US000663.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX PFPI; 2001-488997/53.
XX PT Human genome-derived single exon nucleic acid probes useful for analyzing
XX PT gene expression in human placenta.
```

XX PS Claim 25; SEQ ID NO 16153; 654pp; English.

XX CC The present invention relates to single exon nucleic acid probes (SENP).

XX CC The present sequence is one such probe. The probes are useful for

XX CC producing a microarray for predicting, measuring and displaying gene

XX CC expression in samples derived from human placenta. The probes are useful

XX CC for antenatal diagnosis of human genetic disorders

XX SQ Sequence 1820 BP; 546 A; 406 C; 445 G; 423 T; 0 U; 0 Other;

Query Match 68.2%; Score 15; DB 4; Length 1820;

Best Local Similarity 80.0%; Pred. No. 30;

Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 8 CACUCGUGAGCUCU 22

Db 1774 CACTCGTGAGCTCTT 1760

RESULT 18

ABA49335/c

ID ABA49335 standard; DNA; 1820 BP.

AC ABA49335;

XX 01-FEB-2002 (first entry)

XX Human breast cell single exon nucleic acid probe #8030.

XX Human; microarray; single exon probe; gene expression; breast; disease;

XX cancer; ss.

XX Homo sapiens.

XX WO200157271-A2.

PN 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US000662.

XX 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

PA Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-496933/54.

XX New spatially-addressable set of single exon nucleic acid probes, useful

XX for measuring gene expression in sample derived from human breast,

XX comprises number of single exon nucleic acid probes.

XX Claim 4; SEQ ID NO 8030; 327pp + Sequence Listing; English.

XX The invention relates to a spatially-addressable set of single exon

XX nucleic acid probes for measuring gene expression in a sample derived

XX from human breast and BT 474 cells. The method involves contacting the

XX probes with a collection of detectably labelled nucleic acids derived

XX from mRNA of human breast, and then measuring the label bound to each

XX probe of the microarray. The probes are useful for verifying the

XX expression of regions of genomic DNA predicted to encode proteins. They

XX are useful for gene discovery, and for determining predisposition and/or

XX prognosing breast disease. Gene expression analysis is useful for

XX assessing the toxicity of chemical agents on cells. The microarray of

XX this invention presents a far greater diversity of probes for measuring

XX gene expression, with far less bias than expressed sequence tag

CC microarrays. The method is suitable for rapid production of functional

CC information from genomic sequence. The present sequence is a single exon

CC nucleic acid probe of the invention. Note: The sequence data for this

CC patent did not form part of the printed specification, but was obtained

CC in electronic format directly from WIPO at

CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 1820 BP; 546 A; 406 C; 445 G; 423 T; 0 U; 0 Other;

Query Match 68.2%; Score 15; DB 4; Length 1820;

Best Local Similarity 80.0%; Pred. No. 30;

Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 8 CACUCGUGAGCUCU 22

Db 1774 CACTCGTGAGCTCTT 1760

RESULT 19

ABA34342/c

ID ABA34342 standard; DNA; 1820 BP.

XX ABA34342;

XX 23-JAN-2002 (first entry)

XX Probe #12808 for gene expression analysis in human heart cell sample.

XX Human; gene expression; heart; microarray; vascular system; probe;

XX cardiovascular disease; hypertension; cardiac arrhythmia;

XX congenital heart disease; ss.

XX Homo sapiens.

XX WO200157274-A2.

PN 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US000666.

XX 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

PA Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488899/53.

XX Single exon nucleic acid probes for analyzing gene expression in human

XX hearts.

XX Claim 4; SEQ ID NO 12808; 530pp; English.

XX The present invention relates to single exon nucleic acid probes for

XX measuring human gene expression in a sample derived from human heart. The

XX present sequence is one such probe. The probes may be used for

XX predicting, measuring and displaying gene expression in samples derived

XX from the human heart via microarrays. By measuring gene expression, the

XX probes are useful for predicting, diagnosing, grading, staging,

XX monitoring and prognosing diseases of the human heart and vascular system

XX e.g. cardiovascular disease, hypertension, cardiac arrhythmias and

XX congenital heart disease. Note: The sequence data for this patent did not

XX form part of the printed specification, but was obtained in electronic

XX format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 1820 BP; 546 A; 406 C; 445 G; 423 T; 0 U; 0 Other;

Query Match 68.2%; Score 15; DB 4; Length 1820;
 Best Local Similarity 80.0%; Pred. No. 30;
 Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 8 CACUCGUGAGCUCTT 22
 |||:|||||:
 Db 1774 CACTCGTGAGCTCTT 1760

RESULT 20
 AAK15686/c
 ID AAK15686 standard; DNA; 1820 BP.
 XX
 AC AAK15686;
 XX
 DT 05-NOV-2001 (first entry)
 XX
 DE Human brain expressed single exon probe SEQ ID NO: 15677.
 XX
 DE Human; brain expressed exon; gene expression analysis; probe; microarray;
 KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;
 KW ss.
 KW
 XX Homo sapiens.
 OS
 XX WO200157275-A2.
 PN
 XX 09-AUG-2001.
 PD
 XX 30-JAN-2001; 2001WO-US000667.
 XX
 XX 04-FEB-2000; 2000US-0180312P.
 PR
 PR 26-MAY-2000; 2000US-0207456P.
 PR
 PR 30-JUN-2000; 2000US-00608408.
 PR
 PR 03-AUG-2000; 2000US-00632366.
 PR
 PR 21-SEP-2000; 2000US-0234687P.
 PR
 PR 27-SEP-2000; 2000US-0236359P.
 PR
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 PA
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 PI
 XX WPI; 2001-483446/52.
 XX
 XX Single exon nucleic acid probes for analyzing gene expression in human
 PT brains.
 PT
 XX Example 4; SEQ ID NO 15677; 650pp + Sequence Listing; English.
 PS
 XX The present invention provides a number of single exon nucleic acid
 XX probes which are derived from genomic sequences expressed in the human
 CC brain. They can be used to measure gene expression in brain cell samples,
 CC which may enable the diagnosis and improved treatment of nervous system
 CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
 CC epilepsy and cancers. The present sequence is one of the probes of the
 CC invention
 CC
 XX Sequence 1820 BP; 546 A; 406 C; 445 G; 423 T; 0 U; 0 Other;
 SQ

Query Match 68.2%; Score 15; DB 4; Length 1820;
 Best Local Similarity 80.0%; Pred. No. 30;
 Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 8 CACUCGUGAGCUCTT 22
 |||:|||||:
 Db 1774 CACTCGTGAGCTCTT 1760

RESULT 21
 AAI07869/c
 ID AAI07869 standard; DNA; 1820 BP.
 XX

AC AAI07869;
 XX
 DT 09-OCT-2001 (first entry)
 XX
 DE Probe #7860 used to measure gene expression in human breast sample.
 XX
 KW Probe; human; breast disease; breast cancer; development disorder; ss;
 KW inflammatory disease; proliferative breast disease; non-carcinoma tumour.
 XX
 OS Homo sapiens.
 XX
 XX WO200157270-A2.
 PN
 XX 09-AUG-2001.
 PD
 XX 29-JAN-2001; 2001WO-US000661.
 PF
 XX 04-FEB-2000; 2000US-0180312P.
 PR
 PR 26-MAY-2000; 2000US-0207456P.
 PR
 PR 30-JUN-2000; 2000US-00608408.
 PR
 PR 03-AUG-2000; 2000US-00632366.
 PR
 PR 21-SEP-2000; 2000US-0234687P.
 PR
 PR 27-SEP-2000; 2000US-0236359P.
 PR
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 PA
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 PI
 XX WPI; 2001-476286/51.
 DR
 XX Novel single exon nucleic acid probe used to measuring gene expression in
 PT a human breast.
 PT
 XX Claim 25; SEQ ID NO 7860; 322pp; English.
 PS
 XX The present invention relates to novel single exon nucleic acid probes.
 CC The present sequence is one such probe. The probes are useful for
 CC measuring human gene expression in a human breast sample, where the probe
 CC hybridises at high stringency to a nucleic acid expressed in the human
 CC breast. The probes are useful for predicting, diagnosing, grading,
 CC staging, monitoring and prognosing diseases of the human breast,
 CC particularly those diseases with polygenic aetiology. The diseases
 CC include: breast cancer, disorders of development, inflammatory diseases
 CC of the breast, fibrocystic changes, proliferative breast disease and non-
 CC carcinoma tumours. Note: The sequence data for this patent did not form
 CC part of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 1820 BP; 546 A; 406 C; 445 G; 423 T; 0 U; 0 Other;
 SQ

Query Match 68.2%; Score 15; DB 5; Length 1820;
 Best Local Similarity 80.0%; Pred. No. 30;
 Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 8 CACUCGUGAGCUCTT 22
 |||:|||||:
 Db 1774 CACTCGTGAGCTCTT 1760

RESULT 22
 ABS15429/c
 ID ABS15429 standard; DNA; 1820 BP.
 XX
 AC ABS15429;
 XX
 XX 19-AUG-2002 (first entry)
 DT
 XX Human genome-derived single exon probe ORF from lung SEQ ID No 15420.
 DE
 XX Human; ds; single exon probe; asthma; lung cancer; COPD; ILD;
 KW chronic obstructive pulmonary disease; interstitial lung disease;
 KW familial idiopathic pulmonary fibrosis; neurofibromatosis;

KW tuberosus sclerosis; Gaucher's disease; Niemann-Pick disease;
KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;
KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
KW primary ciliary dyskinesia; pulmonary hypertension;
KW hyaline membrane disease; open reading frame; ORF.
XX
XX
OS Homo sapiens.
XX
XX W0200186003-A2.
XX
XX
XX
XX
XX
XX 30-JAN-2001; 2001WO-US000665.
XX
XX 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2002-114183/15.
XX
XX Spatially-addressable set of single exon nucleic acid probes, used to
XX measure gene expression in human lung samples.
XX
XX Claim 4; SEQ ID NO 15420; 634pp; English.
XX
XX The invention relates to a spatially-addressable set of single exon
XX nucleic acid probes for measuring gene expression in a sample derived
XX from human lung comprising single exon nucleic acid probes having one of
XX 12614 nucleic acid sequences mentioned in the specification, or their
XX complements or the 12387 open reading frames derived from the 12614
XX probes. Also included are a microarray comprising the novel set of probes
XX ; the novel set of probes which hybridise at high stringency to a nucleic
XX acid expressed in the human lung; measuring gene expression in a sample
XX derived from human lung, comprising (a) contacting the array with a
XX collection of detectably labeled nucleic acids derived from human lung
XX mRNA, and (b) measuring the label detectably bound to each probe of the
XX array; identifying exons in a eukaryotic genome, comprising (a)
XX algorithmically predicting at least one exon from genomic sequences of
XX the eukaryote; and (b) detecting specific hybridisation of detectably
XX labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
XX having a fragment identical to the predicted exon, the probe is included
XX in the above mentioned microarray; assigning exons to a single gene,
XX comprising (a) identifying exons from genomic sequence by the method
XX above and (b) measuring the expression of each of the exons in several
XX tissues and/or cell types using hybridisation to a single exon
XX microarrays having a probe with the exon, where a common pattern of
XX expression of the exons in the tissues and/or cell types indicates that
XX the exons should be assigned to a single gene; a peptide comprising one
XX of 12011 sequences, mentioned in the specification, or encoded by the
XX probes/open reading frames (ORF). The probes are used for gene expression
XX analysis, and for identifying exons in a gene, particularly using human
XX lung derived mRNA and for the study of lung diseases such as asthma, lung
XX cancer, chronic obstructive pulmonary disease (COPD), interstitial lung
XX disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,
XX tuberosus sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-
XX Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary
XX histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,
XX Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary
XX dyskinesia, pulmonary hypertension and hyaline membrane disease. The
XX present sequence is a single exon probe open reading frame of the
XX invention. Note: The sequence data for this patent did not form part of
XX the printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 1820 BP; 546 A; 406 C; 445 G; 423 T; 0 U; 0 Other;
Query Match 68.2%; Score 15; DB 6; Length 1820;
Best Local Similarity 80.0%; Pred. No. 30;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
Qy 8 CACUCGUGAGCUCTT 22
Db 1774 CACTCGTGAGCTCTT 1760
|||:||||:||||
RESULT 23
AAI24124/C
ID AAI24124 standard; DNA; 1870 BP.
XX
XX AC AAI24124;
XX
XX DT 12-OCT-2001 (first entry)
XX
XX DE Probe #14057 for gene expression analysis in human cervical cell sample.
XX
XX KW Probe; human; microarray; gene expression; cervical epithelial cell;
XX KW cervical cancer; ss.
XX
XX OS Homo sapiens.
XX
XX PN W0200157278-A2.
XX
XX PD 09-AUG-2001.
XX
XX PF 30-JAN-2001; 2001WO-US000670.
XX
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX DR WPI; 2001-488901/53.
XX
XX PT Human genome-derived single exon nucleic acid probes useful for analyzing
XX gene expression in human cervical epithelial cells.
XX
XX PS Claim 25; SEQ ID NO 14057; 487pp; English.
XX
XX CC The present invention relates to human single exon nucleic acid probes
XX (SENPs). The present sequence is one such probe. The SENPs are derived
XX from human HeLa cells. The SENPs can be used to produce a single exon
XX microarray, which can be used for measuring human gene expression in a
XX sample derived from human cervical epithelial cells. By measuring gene
XX expression, the probes are therefore useful in grading and/or staging of
XX diseases of the cervix, notably cervical cancer. Note: The sequence data
XX for this patent did not form part of the printed specification, but was
XX obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 1870 BP; 568 A; 416 C; 455 G; 431 T; 0 U; 0 Other;
Query Match 68.2%; Score 15; DB 4; Length 1870;
Best Local Similarity 80.0%; Pred. No. 30;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
Qy 8 CACUCGUGAGCUCTT 22
Db 1774 CACTCGTGAGCTCTT 1760
|||:||||:||||


```
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-496933/54.
XX
XX New spatially-addressable set of single exon nucleic acid probes, useful
PT for measuring gene expression in sample derived from human breast,
PT comprises number of single exon nucleic acid probes.
XX
PS Claim 4; SEQ ID NO 9934; 327pp + Sequence Listing; English.
XX
XX The invention relates to a spatially-addressable set of single exon
CC nucleic acid probes for measuring gene expression in a sample derived
CC from human breast and BT 474 cells. The method involves contacting the
CC probes with a collection of detectably labelled nucleic acids derived
CC from mRNA of human breast, and then measuring the label bound to each
CC probe of the microarray. The probes are useful for verifying the
CC expression of regions of genomic DNA predicted to encode proteins. They
CC are useful for gene discovery, and for determining predisposition and/or
CC prognosing breast disease. Gene expression analysis is useful for
CC assessing the toxicity of chemical agents on cells. The microarray of
CC this invention presents a far greater diversity of probes for measuring
CC gene expression, with far less bias than expressed sequence tag
CC microarrays. The method is suitable for rapid production of functional
CC information from genomic sequence. The present sequence is a single exon
CC nucleic acid probe of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1870 BP; 568 A; 416 C; 455 G; 431 T; 0 U; 0 Other;

Query Match 68.2%; Score 15; DB 4; Length 1870;
Best Local Similarity 80.0%; Pred. No. 30;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 8 CACUCGUGAGCUCTT 22
Db |||:|:|:|:|:|
1774 CACTCGTGAGCTCTT 1760

RESULT 27
ID ABA36163/c
AC ABA36163;
XX
XX 23-JAN-2002 (first entry)
DE
DE Probe #14629 for gene expression analysis in human heart cell sample.
XX
XX Human; gene expression; heart; microarray; vascular system; probe;
KW cardiovascular disease; hypertension; cardiac arrhythmia;
KW congenital heart disease; ss.
XX
XX Homo sapiens.
XX
XX WO200157274-A2.
PN
XX 09-AUG-2001.
PD
XX
XX 30-JAN-2001; 2001WO-US000666.
XX
XX 04-FEB-2000; 2000US-0180312P.
PR
XX 26-MAY-2000; 2000US-0207456P.
PR
XX 30-JUN-2000; 2000US-00608408.
PR
XX 03-AUG-2000; 2000US-00632366.
PR
XX 21-SEP-2000; 2000US-0234687P.
PR
XX 27-SEP-2000; 2000US-0236359P.
PR
XX 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488900/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human bone marrow.
PT
XX Example 4; SEQ ID NO 17906; 658pp + Sequence Listing; English.
XX
XX The present invention provides a number of single exon nucleic acid
```

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PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488999/53.
XX
XX Single exon nucleic acid probes for analyzing gene expression in human
PT hearts.
PT
XX Claim 4; SEQ ID NO 14629; 530pp; English.
XX
XX The present invention relates to single exon nucleic acid probes for
CC measuring human gene expression in a sample derived from human heart. The
CC present sequence is one such probe. The probes may be used for
CC predicting, measuring and displaying gene expression in samples derived
CC from the human heart via microarrays. By measuring gene expression, the
CC probes are useful for predicting, diagnosing, grading, staging,
CC monitoring and prognosing diseases of the human heart and vascular system
CC e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
CC congenital heart disease. Note: The sequence data for this patent did not
CC form part of the printed specification, but was obtained in electronic
CC format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1870 BP; 568 A; 416 C; 455 G; 431 T; 0 U; 0 Other;

Query Match 68.2%; Score 15; DB 4; Length 1870;
Best Local Similarity 80.0%; Pred. No. 30;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 8 CACUCGUGAGCUCTT 22
Db |||:|:|:|:|:|
1774 CACTCGTGAGCTCTT 1760

RESULT 28
ID AAK43349/c
AC AAK43349;
XX
XX 06-NOV-2001 (first entry)
DE
DE Human bone marrow expressed single exon probe SEQ ID NO: 17906.
XX
XX Human; bone marrow expressed exon; gene expression analysis; probe;
KW microarray; cancer; leukaemia; lymphoma; myeloma; ss.
XX
XX Homo sapiens.
XX
XX WO200157276-A2.
PN
XX 09-AUG-2001.
PD
XX
XX 30-JAN-2001; 2001WO-US000668.
XX
XX 04-FEB-2000; 2000US-0180312P.
PR
XX 26-MAY-2000; 2000US-0207456P.
PR
XX 30-JUN-2000; 2000US-00608408.
PR
XX 03-AUG-2000; 2000US-00632366.
PR
XX 21-SEP-2000; 2000US-0234687P.
PR
XX 27-SEP-2000; 2000US-0236359P.
PR
XX 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488900/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human bone marrow.
PT
XX Example 4; SEQ ID NO 17906; 658pp + Sequence Listing; English.
XX
XX The present invention provides a number of single exon nucleic acid
```

CC probes which are derived from genomic sequences expressed in the human
 CC bone marrow. They can be used to measure gene expression in bone marrow
 CC samples, which may enable the improved diagnosis and treatment of cancers
 CC such as lymphoma, leukaemia and myeloma. The present sequence is one of
 CC the probes of the invention

XX
 SQ Sequence 1870 BP; 568 A; 416 C; 455 G; 431 T; 0 U; 0 Other;

Query Match 68.2%; Score 15; DB 4; Length 1870;
 Best Local Similarity 80.0%; Pred. No. 30;
 Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 8 CACUCGUGAGCUCTT 22
 |||:|:|:|:|:|:|

Db 1774 CACTCGTGAGCTCTT 1760

RESULT 29
 AAK17541/c
 ID AAK17541 standard; DNA; 1870 BP.
 XX AAK17541;
 AC AAK17541;
 XX
 XX 05-NOV-2001 (first entry)
 XX
 XX Human brain expressed single exon probe SEQ ID NO: 17532.
 DE
 XX Human; brain expressed exon; gene expression analysis; probe; microarray;
 XX Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;
 KW 86.
 KW
 XX Homo sapiens.
 OS
 XX
 XX W0200157275-A2.
 FN
 XX 09-AUG-2001.
 PD
 XX 30-JAN-2001; 2001WO-US000667.
 PF
 XX 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 PA
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2001-483446/52.
 DR
 XX Single exon nucleic acid probes for analyzing gene expression in human
 PT brains.
 XX
 XX Example 4; SEQ ID NO 17532; 650pp + Sequence Listing; English.
 PS
 XX The present invention provides a number of single exon nucleic acid
 CC probes which are derived from genomic sequences expressed in the human
 CC brain. They can be used to measure gene expression in brain cell samples,
 CC which may enable the diagnosis and improved treatment of nervous system
 CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
 CC epilepsy and cancers. The present sequence is one of the probes of the
 CC invention

XX
 SQ Sequence 1870 BP; 568 A; 416 C; 455 G; 431 T; 0 U; 0 Other;

Query Match 68.2%; Score 15; DB 4; Length 1870;
 Best Local Similarity 80.0%; Pred. No. 30;
 Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 8 CACUCGUGAGCUCTT 22

Db 1774 CACTCGTGAGCTCTT 1760
 |||:|:|:|:|:|:|

RESULT 30
 ABS17430/c
 ID ABS17430 standard; DNA; 1870 BP.
 XX
 AC ABS17430;
 XX
 XX 19-AUG-2002 (first entry)
 XX
 XX Human genome-derived single exon probe ORF from lung SEQ ID NO 17421.
 DE
 XX Human; ds; single exon probe; asthma; lung cancer; COPD; IID;
 KW chronic obstructive pulmonary disease; interstitial lung disease;
 KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
 KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
 KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
 KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagenen syndrome;
 KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
 KW primary ciliary dyskinesia; pulmonary hypertension;
 KW hyaline membrane disease; open reading frame; ORF.
 XX
 XX Homo sapiens.
 OS
 XX W0200186003-A2.
 PN
 XX 15-NOV-2001.
 PD
 XX 30-JAN-2001; 2001WO-US000665.
 PF
 XX 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 PA
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2002-114183/15.
 DR
 XX Spatially-addressable set of single exon nucleic acid probes, used to
 PT measure gene expression in human lung samples.
 XX
 XX Claim 4; SEQ ID NO 17421; 634pp; English.
 PS
 XX The invention relates to a spatially-addressable set of single exon
 CC nucleic acid probes for measuring gene expression in a sample derived
 CC from human lung comprising single exon nucleic acid probes having one of
 CC 12614 nucleic acid sequences mentioned in the specification, or their
 CC complements or the 12387 open reading frames derived from the 12614
 CC probes. Also included are a microarray comprising the novel set of probes
 CC; the novel set of probes which hybridise at high stringency to a nucleic
 CC acid expressed in the human lung; measuring gene expression in a sample
 CC derived from human lung, comprising (a) contacting the array with a
 CC collection of detectably labeled nucleic acids derived from human lung
 CC mRNA, and (b) measuring the label detectably bound to each probe of the
 CC array; identifying exons in a eukaryotic genome, comprising (a)
 CC algorithmically predicting at least one exon from genomic sequences of
 CC the eukaryote; and (b) detecting specific hybridisation of detectably
 CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
 CC having a fragment identical to the predicted exon, the probe is included
 CC in the above mentioned microarray; assigning exons to a single gene,
 CC comprising (a) identifying exons from genomic sequence by the method
 CC above and (b) measuring the expression of each of the exons in several
 CC tissues and/or cell types using hybridisation to a single exon
 CC microarrays having a probe with the exon, where a common pattern of
 CC expression of the exons in the tissues and/or cell types indicates that

CC the exons should be assigned to a single gene; a peptide comprising one
 CC of 12011 sequences, mentioned in the specification, or encoded by the
 CC probes/open reading frames (ORF). The probes are used for gene expression
 CC analysis, and for identifying exons in a gene, particularly using human
 CC lung derived mRNA and for the study of lung diseases such as asthma, lung
 CC cancer, chronic obstructive pulmonary disease (COPD), interstitial lung
 CC disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,
 CC tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-
 CC Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary
 CC histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,
 CC Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary
 CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The
 CC present sequence is a single exon probe open reading frame of the
 CC invention. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 1870 BP; 568 A; 416 C; 455 G; 431 T; 0 U; 0 Other;
 Query Match 68.2%; Score 15; DB 6; Length 1870;
 Best Local Similarity 80.0%; Pred. No. 30;
 Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 8 CACUCGUGAGCTCTT 22
 Db 1774 CACTCGTGAGCTCTT 1760
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 Job time : 455 secs

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OM nucleic - nucleic search, using sw model

Run on: July 20, 2005, 22:37:01 ; Search time 3090 Seconds
(without alignments)
271.008 Million cell updates/sec

Title: US-10-848-737-1

Perfect score: 22

Sequence: 1 gugaacucacugagacutt 22

Scoring table:

OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 34239544 seqs, 19032134700 residues

Word size : 0

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 300 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_hlc:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gse1:*

9: gb_gse2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	17	77.3	1344	4	BG917388
C 2	16	72.7	200	7	CF296001
C 3	16	72.7	206	7	CF29826
C 4	16	72.7	245	7	CF298930
C 5	16	72.7	270	2	BE228712
C 6	16	72.7	272	7	CF295034
C 7	16	72.7	273	7	CF299062
C 8	16	72.7	276	7	CF300491
C 9	16	72.7	277	7	CF300259
C 10	16	72.7	281	7	CF298981
C 11	16	72.7	283	7	CF298536
C 12	16	72.7	311	7	CF294911
C 13	16	72.7	313	6	CF299992
C 14	16	72.7	315	6	CB668085
C 15	16	72.7	321	7	CF300735
C 16	16	72.7	325	7	CF300267
C 17	16	72.7	321	7	CF334972
C 18	16	72.7	324	7	CF301775
C 19	16	72.7	326	7	CF295092
C 20	16	72.7	329	7	CF300479
C 21	16	72.7	326	7	CF298299
C 22	16	72.7	330	7	CF301705
C 23	16	72.7	340	7	CF299101
C 24	16	72.7	342	7	CF294601
C 25	16	72.7	343	7	CF300860
C 26	16	72.7	349	7	CF302308
C 27	16	72.7	350	4	BI810487
C 28	16	72.7	350	7	CF333939
C 29	16	72.7	351	7	CF300157
C 30	16	72.7	352	7	CF301059
C 31	16	72.7	353	7	CF294542
C 32	16	72.7	358	7	CF293314
C 33	16	72.7	358	7	CF301046
C 34	16	72.7	359	7	CF301825
C 35	16	72.7	360	7	CF295099
C 36	16	72.7	361	7	CF293177
C 37	16	72.7	361	7	CF333477
C 38	16	72.7	363	7	CF294625
C 39	16	72.7	364	4	BI797027
C 40	16	72.7	364	7	CF294049
C 41	16	72.7	364	7	CF300473
C 42	16	72.7	365	7	CF302540
C 43	16	72.7	366	7	CF300089
C 44	16	72.7	367	7	CF334002
C 45	16	72.7	368	7	CF293465
C 46	16	72.7	368	7	CF294528
C 47	16	72.7	369	7	CF294797
C 48	16	72.7	372	7	CF334668
C 49	16	72.7	373	7	CF298619
C 50	16	72.7	373	7	CF299944
C 51	16	72.7	381	7	CF301512
C 52	16	72.7	382	6	CA882915
C 53	16	72.7	388	7	CF333248
C 54	16	72.7	389	2	BE228607
C 55	16	72.7	389	7	CF296172
C 56	16	72.7	389	7	CF302115
C 57	16	72.7	391	7	CF279865
C 58	16	72.7	394	7	CF292628
C 59	16	72.7	396	7	CF293499
C 60	16	72.7	397	7	CF295674
C 61	16	72.7	398	7	CF281031
C 62	16	72.7	400	7	CF293653
C 63	16	72.7	400	7	CF301091
C 64	16	72.7	402	7	CF292898
C 65	16	72.7	402	7	CF301882
C 66	16	72.7	402	7	CF333799
C 67	16	72.7	404	7	CF293571
C 68	16	72.7	405	7	CF292038
C 69	16	72.7	405	7	CF291160
C 70	16	72.7	407	7	CF295956
C 71	16	72.7	409	7	CF297322
C 72	16	72.7	412	7	CF302167
C 73	16	72.7	414	7	CF292634
C 74	16	72.7	415	7	CF292393
C 75	16	72.7	415	7	CF317419
C 76	16	72.7	417	7	CF302841
C 77	16	72.7	417	7	CF337043
C 78	16	72.7	419	7	CF310192
C 79	16	72.7	420	6	CA752917
C 80	16	72.7	420	6	CA752923
C 81	16	72.7	421	6	CA752899
C 82	16	72.7	421	6	CF293078
C 83	16	72.7	423	7	CF301435
C 84	16	72.7	424	2	AW069961
C 85	16	72.7	427	7	CF293708
C 86	16	72.7	427	7	CF300099
C 87	16	72.7	427	7	CF302576
C 88	16	72.7	428	7	CF301852
C 89	16	72.7	431	7	CF293115
C 90	16	72.7	431	7	CF295077
C 91	16	72.7	431	7	CF335603
C 92	16	72.7	432	7	CF294230
C 93	16	72.7	433	4	CF299231
C 94	16	72.7	434	4	BM038487
C 95	16	72.7	435	4	BI795494
C 96	16	72.7	435	7	CF297684
C 97	16	72.7	436	7	CF333485

CF300860 7LEAF--05
CF302308 7LEAF--07
BI810487 J009E03 O
CF333939 JMT--03-A
CF300157 7LEAF--04
CF301059 7LEAF--05
CF294542 3ODGS--04
CF293314 3ODGS--02
CF301046 7LEAF--05
CF301825 7LEAF--06
CF295099 3ODGS--04
CF293177 3ODGS--02
CF333477 JMT--02-G
CF294625 3ODGS--04
BI797027 H062C08 E
CF294049 3ODGS--03
CF300473 7LEAF--04
CF302540 7LEAF--08
CF300089 7LEAF--04
CF334002 JMT--03-C
CF293465 3ODGS--02
CF294528 3ODGS--04
CF294797 3ODGS--04
CF334668 JMT--04-A
CF298619 7LEAF--02
CF301512 7LEAF--06
CA882915 SSHD19 R1
CF333248 JMT--02-B
BE228607 98AS2865
CF296172 3ODGS--06
CF302115 7LEAF--07
CF29865 14ETL--06
CF292628 3ODGS--01
CF293499 3ODGS--02
CF295674 3ODGS--05
CF281031 14ETL--07
CF293653 3ODGS--02
CF301091 7LEAF--05
CF292898 3ODGS--01
CF301882 7LEAF--06
CF333799 JMT--02-N
CF293571 3ODGS--02
CF292038 14ROOT--0
CF291160 14ROOT--0
CF295956 3ODGS--06
CF297322 3ODGS--08
CF302167 7LEAF--07
CF292634 3ODGS--01
CF292393 3ODGS--01
CF317419 HD--07-B1
CF302841 7LEAF--08
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CF310192 ABF--04-L
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CA752923 JSYL471 r
CA752899 JSYL374 r
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CF293115 3ODGS--02
CF295077 3ODGS--04
CF335603 JMT--05-F
CF294230 3ODGS--03
CF299231 7LEAF--03
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BI795494 H023H07 E
CF297684 3ODGS--08
CF333485 JMT--02-G

C 98	16	72.7	437	7	CF300287	7LEAF--04	C 171	16	72.7	491	7	CF335971	JMT--05-N
C 99	16	72.7	438	7	CF336757	JMT--06-I	C 172	16	72.7	492	7	CF335871	JMT--05-L
C 100	16	72.7	439	7	CF336454	JMT--06-I	C 173	16	72.7	493	7	CF302098	7LEAF--07
C 101	16	72.7	440	4	BI810469	J009B04 O	C 174	16	72.7	493	7	CF336032	JMT--05-P
C 102	16	72.7	443	7	CF298634	7LEAF--02	C 175	16	72.7	495	7	CF294456	30DGS--03
C 103	16	72.7	443	7	CF326605	JMT1--06-F	C 176	16	72.7	495	7	CF301786	7LEAF--06
C 104	16	72.7	444	7	CF296710	30DGS--07	C 177	16	72.7	495	7	CF336909	JMT--07-C
C 105	16	72.7	447	7	CF300126	7LEAF--04	C 178	16	72.7	496	7	CF292748	30DGS--01
C 106	16	72.7	447	7	CF334006	JMT--03-C	C 179	16	72.7	496	7	CF299949	7LEAF--04
C 107	16	72.7	447	7	CF335012	JMT--04-I	C 180	16	72.7	496	7	CF336522	JMT--06-J
C 108	16	72.7	448	7	CF292622	30DGS--01	C 181	16	72.7	497	7	CF300189	7LEAF--04
C 109	16	72.7	448	7	CF298719	7LEAF--02	C 182	16	72.7	497	7	CF335479	JMT--05-C
C 110	16	72.7	452	7	CF299236	7LEAF--02	C 183	16	72.7	498	7	CF294477	30DGS--04
C 111	16	72.7	454	7	CF307856	ABF--01-H	C 184	16	72.7	498	7	CF297419	30DGS--08
C 112	16	72.7	454	7	CF298335	7LEAF--01	C 185	16	72.7	499	5	BQ907486	P007C11 O
C 113	16	72.7	455	7	CF333435	7LEAF--02-F	C 186	16	72.7	499	7	CF296926	30DGS--07
C 114	16	72.7	459	7	CF295831	30DGS--05	C 187	16	72.7	499	7	CF299465	7LEAF--03
C 115	16	72.7	459	7	CF302341	7LEAF--07	C 188	16	72.7	499	7	CF302481	7LEAF--08
C 116	16	72.7	460	4	BI807599	A006C09 O	C 189	16	72.7	499	7	CF332788	JMT--01-G
C 117	16	72.7	461	7	CF195895	A2b12.1 A	C 190	16	72.7	500	7	CF332942	JMT--01-K
C 118	16	72.7	461	7	CF311539	ABF--06-M	C 191	16	72.7	500	7	CF335956	JMT--05-N
C 119	16	72.7	462	7	CF295701	30DGS--05	C 192	16	72.7	500	7	CF336502	JMT--06-J
C 120	16	72.7	462	7	CF297362	30DGS--08	C 193	16	72.7	501	7	CF293284	30DGS--02
C 121	16	72.7	462	7	CF299260	7LEAF--03	C 194	16	72.7	501	7	CF300694	7LEAF--05
C 122	16	72.7	463	7	CF295676	30DGS--05	C 195	16	72.7	501	7	CF334025	JMT--03-C
C 123	16	72.7	464	7	CF295075	30DGS--04	C 196	16	72.7	501	7	CF334152	JMT--03-F
C 124	16	72.7	464	7	CF298102	7LEAF--01	C 197	16	72.7	501	7	CF335291	JMT--04-O
C 125	16	72.7	466	7	CF333098	JMT--01-N	C 198	16	72.7	501	7	CF335896	JMT--05-M
C 126	16	72.7	466	7	CF336355	JMT--06-G	C 199	16	72.7	502	5	BQ529578	h12-c3.8e
C 127	16	72.7	467	7	CF295382	30DGS--05	C 200	16	72.7	502	7	CF333698	JMT--02-L
C 128	16	72.7	467	7	CF299470	7LEAF--07	C 201	16	72.7	503	7	CF308990	ABF--03-A
C 129	16	72.7	467	7	CF332819	JMT--01-H	C 202	16	72.7	503	7	CF336371	JMT--06-G
C 130	16	72.7	467	7	CF338041	JMT--08-L	C 203	16	72.7	504	7	CF302018	7LEAF--07
C 131	16	72.7	469	7	CF300208	7LEAF--04	C 204	16	72.7	504	7	CF302471	7LEAF--08
C 132	16	72.7	470	7	CF298227	7LEAF--01	C 205	16	72.7	504	7	CF312560	ABF--08-F
C 133	16	72.7	470	7	CF302203	7LEAF--07	C 206	16	72.7	504	7	CF337598	JMT--08-B
C 134	16	72.7	472	7	CF297460	30DGS--08	C 207	16	72.7	505	1	AA753360	97AS2393
C 135	16	72.7	472	7	CF299893	7LEAF--04	C 208	16	72.7	505	5	BQ907567	P008G11 O
C 136	16	72.7	472	7	CF333611	JMT--02-J	C 209	16	72.7	505	7	CF301004	7LEAF--05
C 137	16	72.7	473	7	CF334916	JMT--04-G	C 210	16	72.7	505	7	CF335313	JMT--04-P
C 138	16	72.7	474	7	CF311574	ABF--06-N	C 211	16	72.7	505	7	CF337248	JMT--07-J
C 139	16	72.7	474	7	CF334359	JMT--03-K	C 212	16	72.7	506	7	CF296585	30DGS--07
C 140	16	72.7	474	7	CF335615	JMT--05-F	C 213	16	72.7	506	7	CF333254	JMT--02-B
C 141	16	72.7	477	4	BI809799	G003A04 O	C 214	16	72.7	506	7	CF336913	JMT--07-C
C 142	16	72.7	478	7	CF333330	JMT--02-D	C 215	16	72.7	507	7	CF295579	30DGS--08
C 143	16	72.7	478	7	CF338043	JMT--08-L	C 216	16	72.7	507	7	CF295579	30DGS--05
C 144	16	72.7	479	2	BF430561	OG02C02T3	C 217	16	72.7	507	7	CF302633	7LEAF--03-D
C 145	16	72.7	479	7	CF302933	7LEAF--08	C 218	16	72.7	508	7	CF334079	JMT--02-I
C 146	16	72.7	480	4	BM419049	R008F02 O	C 219	16	72.7	508	7	CF333590	JMT--04-G
C 147	16	72.7	480	7	CF333127	JMT--01-O	C 220	16	72.7	509	7	CF334927	JMT--04-G
C 148	16	72.7	481	7	CF312849	ABF--08-M	C 221	16	72.7	509	7	CF312061	ABF--07-J
C 149	16	72.7	481	7	CF335083	JMT--04-J	C 222	16	72.7	509	7	CF332812	JMT--01-H
C 150	16	72.7	484	7	CF297887	7LEAF--01	C 223	16	72.7	509	7	CF335309	JMT--04-P
C 151	16	72.7	484	7	CF302376	7LEAF--07	C 224	16	72.7	509	7	CF336057	JMT--05-P
C 152	16	72.7	484	7	CF334479	JMT--03-M	C 225	16	72.7	509	7	CF337639	JMT--08-C
C 153	16	72.7	484	7	CF335350	JMT--04-P	C 226	16	72.7	510	7	CF333207	JMT--02-A
C 154	16	72.7	485	7	CF302641	7LEAF--08	C 227	16	72.7	510	7	CF336446	JMT--06-I
C 155	16	72.7	485	7	CF336484	JMT--06-I	C 228	16	72.7	511	2	BE229988	99AS225 R
C 156	16	72.7	486	7	CF295252	30DGS--05	C 229	16	72.7	511	7	CF300116	7LEAF--04
C 157	16	72.7	486	7	CF297412	30DGS--08	C 230	16	72.7	511	7	CF337862	JMT--08-H
C 158	16	72.7	486	7	CF299637	7LEAF--03	C 231	16	72.7	512	7	CF294297	30DGS--03
C 159	16	72.7	486	7	CF336999	JMT--07-E	C 232	16	72.7	512	7	CF297126	30DGS--07
C 160	16	72.7	486	7	CF337803	JMT--08	C 233	16	72.7	513	7	CF299626	7LEAF--03
C 161	16	72.7	487	7	CF302594	7LEAF--08	C 234	16	72.7	513	7	CF336924	JMT--07-C
C 162	16	72.7	487	7	CF332798	JMT--01-H	C 235	16	72.7	514	7	CF295780	30DGS--05
C 163	16	72.7	487	7	CF334015	JMT--03-C	C 236	16	72.7	514	7	CF298176	7LEAF--01
C 164	16	72.7	487	7	CF335223	JMT--04-N	C 237	16	72.7	514	7	CF302889	7LEAF--08
C 165	16	72.7	487	7	CF335874	JMT--05-L	C 238	16	72.7	514	7	CR286903	CR286903
C 166	16	72.7	487	7	CF335893	JMT--05-L	C 239	16	72.7	515	7	CF298884	7LEAF--02
C 167	16	72.7	488	7	CF333761	JMT--02-M	C 240	16	72.7	516	7	CF337361	JMT--07-M
C 168	16	72.7	488	7	CF334521	JMT--03-N	C 241	16	72.7	517	7	CF332559	JMT--01-C
C 169	16	72.7	490	7	CF294832	30DGS--04	C 242	16	72.7	519	4	BM419793	BM419793
C 170	16	72.7	490	7	CF335453	JMT--05-C	C 243	16	72.7	520	4	BM419601	BM419601

CF298930/c	CF298930	245 bp	mRNA	linear	EST 15-AUG-2000
LOCUS	7LEAF--02-K15.g1	Rice leaf	plasmid	cDNA library II (7LEAF)	Oryza
DEFINITION	sativa (japonica cultivar-group)	cDNA clone 7LEAF--02-K15,	mrna		
		sequence.			
ACCESSION	CF298930				
VERSION	CF298930.1	GI:33670691			
KEYWORDS	EST.				
SOURCE	Oryza sativa (japonica cultivar-group)				
ORGANISM	Oryza sativa (japonica cultivar-group)				
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzae; Oryza.				
REFERENCE	1 (bases 1 to 245)				
AUTHORS	Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.				
TITLE	Large-scale Sequencing Analysis of Rice ESTs				
JOURNAL	Unpublished (2003)				
COMMENT	Contact: Nahm B.H.				
	Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongui University				
	Yongin, Kyeonggi, Korea				
	Tel: 82 31 330 6193				
	Fax: 82 31 321 6355				
	Email: bhnaheggbio.com, bhnaheggbio.myongji.ac.kr.				
FEATURES	Location/Qualifiers				
source	1..245				
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	/cultivar="Nackdong"				
	/db_xref="taxon:39947"				
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	/tissue_type="leaf"				
	/dev_stage="7 days after germination"				
	/lab_host="E.coli DH10B"				
	/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"				
	/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."				
ORIGIN					
Query Match	72.7%;	Score 16;	DB 7;	Length 245;	
Best Local Similarity	75.0%;	Pred. No. 37;			
Matches	12;	Conservative	4;	Mismatches	0;
				Indels	0;
				Gaps	0;
QY	6	CUCACUCGUGAGCUCT	21		
	: : : : : : : : :				
Db	133	CTCACTCGTGAGCTCT	118		
RESULT 5					
BE228712					
LOCUS	BE228712	270 bp	mRNA	linear	EST 07-JUL-2000
DEFINITION	98AS3025 Rice Immature Seed	Lambda ZAPII cDNA Library	Oryza sativa		
	(indica cultivar-group)	cDNA clone 98AS3025,	mrna		
ACCESSION	BE228712				
VERSION	BE228712.1	GI:8954906			
KEYWORDS	EST.				
SOURCE	Oryza sativa (indica cultivar-group)				
ORGANISM	Oryza sativa (indica cultivar-group)				
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzae; Oryza.				
REFERENCE	1 (bases 1 to 270)				
AUTHORS	Nahm,B.H., Kim,J.K., Cheong,J.J., Kim,S.I., Hahn,T.R., Moon,E.P., Kim,W.T., Kim,W.Y., Yang,M.S., Park,R.D., Sohn,U.I., Kang,K.Y., Lee,M.C. and Eun,M.Y.				
TITLE	Large-scale Sequencing Analysis of ESTs from Rice Immature Seed				
JOURNAL	Unpublished (1998)				
COMMENT	Contact: Eun M.Y.				
	Department of Cytogenetics				
	National Inst. of Agri. Sci. and Tech, RDA				
	Swon, Kyungqido, Korea				
CF299826/c	CF299826	206 bp	mRNA	linear	EST 15-AUG-2003
LOCUS	7LEAF--04-A01.g1	Rice leaf	plasmid	cDNA library II (7LEAF)	Oryza
DEFINITION	sativa (japonica cultivar-group)	cDNA clone 7LEAF--04-A01,	mrna		
		sequence.			
ACCESSION	CF299826				
VERSION	CF299826.1	GI:33671587			
KEYWORDS	EST.				
SOURCE	Oryza sativa (japonica cultivar-group)				
ORGANISM	Oryza sativa (japonica cultivar-group)				
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzae; Oryza.				
REFERENCE	1 (bases 1 to 206)				
AUTHORS	Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.				
TITLE	Large-scale Sequencing Analysis of Rice ESTs				
JOURNAL	Unpublished (2003)				
COMMENT	Contact: Nahm B.H.				
	Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongui University				
	Yongin, Kyeonggi, Korea				
	Tel: 82 31 330 6193				
	Fax: 82 31 321 6355				
	Email: bhnaheggbio.com, bhnaheggbio.myongji.ac.kr.				
FEATURES	Location/Qualifiers				
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	/cultivar="Nackdong"				
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	/clone="7LEAF--04-A01"				
	/tissue_type="leaf"				
	/dev_stage="7 days after germination"				
	/lab_host="E.coli DH10B"				

Tel: 82 331 290 0301
 Fax: 82 331 290 0307
 Email: myeun@sun20.asti.re.kr.
 Location/Qualifiers

FEATURES

source

1. .270
 /organism="Oryza sativa (indica cultivar-group)"
 /mol_type="mRNA"
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 /dev_stage="5 days after pollination"
 /lab_host="E. coli SOLR"
 /clone_lib="Rice Immature Seed Lambda ZAPII cDNA Library"
 /note="Vector: phuescript SK(+); Site 1: EcoRI; Site 2:
 XhoI; Directional cDNA library inserted into lambda ZAPII
 vector at 5' end with EcoRI and 3' end with Xho I site."

ORIGIN

Query Match 72.7%; Score 16; DB 2; Length 270;
 Best Local Similarity 75.0%; Pred. No. 37;
 Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CUCACUCGUGAGCUCT 21

Db 32 CTCACCTGCTGAGCTCT 47

RESULT 6

CF295034/c

LOCUS

DEFINITION 30DGS--04-M16.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza sativa (japonica cultivar-group) cDNA clone 30DGS--04-M16, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 272)
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 321 6355
 Fax: 82 31 321 6355
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

source

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 /mol_type="mRNA"
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 with oligoribonucleotides and then used as templates for
 RT-PCR."

ORIGIN

Query Match 72.7%; Score 16; DB 7; Length 272;
 Best Local Similarity 75.0%; Pred. No. 37;
 Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CUCACUCGUGAGCUCT 21

Db 129 CTCACCTGCTGAGCTCT 114

RESULT 7

CF299062/c

LOCUS

DEFINITION

KEYWORDS

SOURCE

ORGANISM

7LEAF--02-O13.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--02-O13, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

CF299062 273 bp mRNA linear EST 15-AUG-2003

CF299062.1 GI:33670823

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 273)
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 321 6355
 Fax: 82 31 321 6355
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

source

1. .273
 /organism="Oryza sativa (japonica cultivar-group)"
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 /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
 /note="vector: PCR4-TORO; Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

ORIGIN

Query Match 72.7%; Score 16; DB 7; Length 273;
 Best Local Similarity 75.0%; Pred. No. 37;
 Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CUCACUCGUGAGCUCT 21

Db 182 CTCACCTGCTGAGCTCT 167

RESULT 8

CF300491/c

LOCUS

DEFINITION

KEYWORDS

SOURCE

ORGANISM

CF300491 273 bp mRNA linear EST 15-AUG-2003
 7LEAF--04-P09.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--04-P09, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

CF300491.1 GI:33672252

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

AUTHORS

1 (bases 1 to 273)
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,


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Query Match      72.7%; Score 16; DB 7; Length 321;
Best Local Similarity 75.0%; Pred. No. 37;
Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      6  CUACACUGGAGGCUCT 21
       1:||||:||||:||||:|
Db      261 CTCACCTCGTGAGCTCT 246

RESULT 17
CF334972/c
LOCUS      321 bp      mRNA      linear      EST 18-AUG-2003
DEFINITION JMT--04-H11.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
            JMT--04-H11, mRNA sequence.
ACCESSION  CF334972
VERSION     CF334972.1 GI:33818275
KEYWORDS   EST.
SOURCE     Oryza sativa (japonica cultivar-group)
ORGANISM   Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE  1 (bases 1 to 321)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             source
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     1..321
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     /tissue_type="leaf"
     /dev_stage="14 days after germination"
     /lab_host="E.coli DH10B"
     /clone_lib="AtJMT-overexpressing transgenic rice plasmid
     cDNA library (JMT)"
     /notes="Vector: PCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
     was reverse transcribed and then used for PCR. mRNA was
     prepared from Arabidopsis Jasmonate Carboxyl
     methyltransferase overexpression line."

ORIGIN
Query Match      72.7%; Score 16; DB 7; Length 321;
Best Local Similarity 75.0%; Pred. No. 37;
Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      6  CUACACUGGAGGCUCT 21
       1:||||:||||:||||:|
Db      261 CTCACCTCGTGAGCTCT 246

RESULT 18
CF3301775/c
LOCUS      324 bp      mRNA      linear      EST 15-AUG-2003
DEFINITION 7LEAF--06-M05.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--06-M05, mRNA
            sequence.
ACCESSION  CF3301775
VERSION     CF3301775.1 GI:33673536
KEYWORDS   EST.
SOURCE     Oryza sativa (japonica cultivar-group)
ORGANISM   Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE  1 (bases 1 to 324)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             source
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     1..324
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     /tissue_type="leaf"
     /dev_stage="7 days after germination"
     /lab_host="E.coli DH10B"
     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
     /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
     with oligoribonucleotides and then used as templates for
     RT-PCR."

ORIGIN
Query Match      72.7%; Score 16; DB 7; Length 324;
Best Local Similarity 75.0%; Pred. No. 37;
Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      6  CUACACUGGAGGCUCT 21
       1:||||:||||:||||:|
Db      312 CTCACCTCGTGAGCTCT 297

RESULT 19
CF295092/c
LOCUS      326 bp      mRNA      linear      EST 14-AUG-2003
DEFINITION 30DGS--04-N22.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
            sativa (japonica cultivar-group) cDNA clone 30DGS--04-N22, mRNA
            sequence.
ACCESSION  CF295092
VERSION     CF295092.1 GI:33664125
KEYWORDS   EST.
SOURCE     Oryza sativa (japonica cultivar-group)
ORGANISM   Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE  1 (bases 1 to 326)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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     /mol_type="mRNA"
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     /db_xref="taxon:39947"

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DEFINITION	7LEAF--01-K01.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--01-K01, mRNA sequence.
ACCESSION	CF298299
VERSION	CF298299.1 GI:33670060
KEYWORDS	EST.
SOURCE	Oryza sativa (japonica cultivar-group)
ORGANISM	Oryza sativa (japonica cultivar-group)
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaeae; Oryza.
AUTHORS	Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE	Large-scale Sequencing Analysis of Rice ESTs
JOURNAL	Unpublished (2003)
COMMENT	Contact: Nahm B.H.
FEATURES	<p>1 (bases 1 to 329)</p> <p>Source</p> <p>Location/Qualifiers</p> <p>1..329</p> <p>/organism="Oryza sativa (japonica cultivar-group)"</p> <p>/mol_type="mRNA"</p> <p>/cultivar="Nackdong"</p> <p>/db_xref="taxon:39947"</p> <p>/clone="7LEAF--01-K01"</p> <p>/tissue_type="leaf"</p> <p>/dev_stage="7 days after germination"</p> <p>/lab_host="E.coli DH10B"</p> <p>/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"</p> <p>/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."</p>
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Best Local Similarity	75.0%; Pred. No. 37;
Matches	12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY	6 CUACUCUGAGGAGCTCT 21
Db	311 CTCACCTCGTGAGCTCT 296
RESULT 22	
CF301705/c	
LOCUS	CF301705.1 GI:33673466
DEFINITION	7LEAF--06-K17.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--06-K17, mRNA sequence.
ACCESSION	CF301705
VERSION	CF301705.1 GI:33673466
KEYWORDS	EST.
SOURCE	Oryza sativa (japonica cultivar-group)
ORGANISM	Oryza sativa (japonica cultivar-group)
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaeae; Oryza.
AUTHORS	Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE	Large-scale Sequencing Analysis of Rice ESTs
JOURNAL	Unpublished (2003)
COMMENT	Contact: Nahm B.H.
FEATURES	<p>1 (bases 1 to 330)</p> <p>Source</p> <p>Location/Qualifiers</p> <p>1..326</p> <p>/organism="Oryza sativa (japonica cultivar-group)"</p> <p>/mol_type="mRNA"</p> <p>/cultivar="Nackdong"</p> <p>/db_xref="taxon:39947"</p> <p>/clone="7LEAF--04-017"</p> <p>/tissue_type="leaf"</p> <p>/dev_stage="7 days after germination"</p> <p>/lab_host="E.coli DH10B"</p> <p>/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"</p> <p>/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."</p>
ORIGIN	
Query Match	72.7%; Score 16; DB 7; Length 326;
Best Local Similarity	75.0%; Pred. No. 37;
Matches	12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY	6 CUACUCUGAGGAGCTCT 21
Db	308 CTCACCTCGTGAGCTCT 293
RESULT 20	
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DEFINITION	7LEAF--04-017.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--04-017, mRNA sequence.
ACCESSION	CF300479
VERSION	CF300479.1 GI:33672240
KEYWORDS	EST.
SOURCE	Oryza sativa (japonica cultivar-group)
ORGANISM	Oryza sativa (japonica cultivar-group)
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaeae; Oryza.
AUTHORS	Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE	Large-scale Sequencing Analysis of Rice ESTs
JOURNAL	Unpublished (2003)
COMMENT	Contact: Nahm B.H.
FEATURES	<p>1 (bases 1 to 326)</p> <p>Source</p> <p>Location/Qualifiers</p> <p>1..326</p> <p>/organism="Oryza sativa (japonica cultivar-group)"</p> <p>/mol_type="mRNA"</p> <p>/cultivar="Nackdong"</p> <p>/db_xref="taxon:39947"</p> <p>/clone="7LEAF--04-017"</p> <p>/tissue_type="leaf"</p> <p>/dev_stage="7 days after germination"</p> <p>/lab_host="E.coli DH10B"</p> <p>/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"</p> <p>/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."</p>
ORIGIN	
Query Match	72.7%; Score 16; DB 7; Length 326;
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Matches	12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY	6 CUACUCUGAGGAGCTCT 21
Db	308 CTCACCTCGTGAGCTCT 293
RESULT 21	
CF298299/c	
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DEFINITION	7LEAF--01-K01.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--01-K01, mRNA sequence.
ACCESSION	CF298299
VERSION	CF298299.1 GI:33670060
KEYWORDS	EST.
SOURCE	Oryza sativa (japonica cultivar-group)
ORGANISM	Oryza sativa (japonica cultivar-group)
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaeae; Oryza.
AUTHORS	Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE	Large-scale Sequencing Analysis of Rice ESTs
JOURNAL	Unpublished (2003)
COMMENT	Contact: Nahm B.H.
FEATURES	<p>1 (bases 1 to 329)</p> <p>Source</p> <p>Location/Qualifiers</p> <p>1..329</p> <p>/organism="Oryza sativa (japonica cultivar-group)"</p> <p>/mol_type="mRNA"</p> <p>/cultivar="Nackdong"</p> <p>/db_xref="taxon:39947"</p> <p>/clone="7LEAF--01-K01"</p> <p>/tissue_type="leaf"</p> <p>/dev_stage="7 days after germination"</p> <p>/lab_host="E.coli DH10B"</p> <p>/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"</p> <p>/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."</p>
ORIGIN	
Query Match	72.7%; Score 16; DB 7; Length 329;
Best Local Similarity	75.0%; Pred. No. 37;
Matches	12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY	6 CUACUCUGAGGAGCTCT 21
Db	311 CTCACCTCGTGAGCTCT 296

JOURNAL
COMMENT

Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES

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/tissue_type="leaf"
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ORIGIN

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Best Local Similarity 75.0%; Pred. No. 37;
Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 6 CUCACUCGUGAGCUCT 21

|:|:|:|:|:|:|

Db 325 CTCACCTCGTGAGCTCT 310

RESULT 26

CF302308/c

LOCUS

DEFINITION
7LEAF--07-L05.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa (japonica cultivar-group) cDNA clone 7LEAF--07-L05, mRNA
sequence.

ACCESSION CF302308 1 GI:33674069

VERSION

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 349)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

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FEATURES

source

1. 349
/organism="Oryza sativa (japonica cultivar-group)"
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/dev_stage="7 days after germination"
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/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

ORIGIN

Query Match 72.7%; Score 16; DB 7; Length 349;
Best Local Similarity 75.0%; Pred. No. 37;
Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 6 CUCACUCGUGAGCUCT 21

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Db 331 CTCACCTCGTGAGCTCT 316

RESULT 27

BI810487

LOCUS

DEFINITION
BI810487 Oryza sativa mature leaf library induced by M.grisea Oryza
sativa cDNA clone J009E03, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 350)

AUTHORS

Dong, H.T., Li, D.B., Zhuang, X.F., Dai, C.G., Sun, L.X., Pei, Y.X.,

Wu, H.F., Jiang, Y.X., Yu, P.C., Gao, Q.K. and Lou, Y.C.

A Gene Expression Screen in Oryza sativa

Unpublished (2001)

Contact: Haitao Dong, Debao Li

Bioinformatics and Gene Network Research Group

Zhejiang University

Kaixuan Road 268#, Hangzhou, Zhejiang, P.R.China

Tel: 0086-571-86932051

Fax: 0086-571-86961525

Email: webmaster@estarray.org, URL: http://www.estarray.org

Seq primer: M3 forward primer.

FEATURES

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M.grisea"
/note="Vector: pSport2"

ORIGIN

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Best Local Similarity 75.0%; Pred. No. 37;
Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 6 CUCACUCGUGAGCUCT 21

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Db 11 CTCACCTCGTGAGCTCT 26

RESULT 28

CF333939/c

LOCUS

DEFINITION
JMT--03-A17.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

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OM nucleic - nucleic search, using sw model

Run on: July 20, 2005, 22:44:51 ; Search time 128 Seconds
(without alignments)
281.235 Million cell updates/sec

Title: US-10-848-737-1

Perfect score: 22

Sequence: 1 gugaacucacugagacuctt 22

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 1202784 seqs, 818138359 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 300 summaries

Database : Issued Patents NA.*

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- 5: /cgn2_6/ptodata/1/ina/PTUS_COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 1	15	68.2	234884	4	US-09-949-016-16420
C 2	14	63.6	348	3	Sequence 16420, A
C 3	14	63.6	428	4	Sequence 2127, Ap
C 4	14	63.6	428	4	Sequence 8994, Ap
C 5	14	63.6	428	4	Sequence 24276, A
C 6	14	63.6	3170	4	Sequence 3849, Ap
C 7	14	63.6	4329	4	Sequence 2051, Ap
C 8	14	63.6	300598	4	Sequence 11868, A
C 9	14	63.6	302604	4	Sequence 14589, A
C 10	14	63.6	302604	4	Sequence 14589, A
C 11	14	63.6	308362	4	Sequence 14589, A
C 12	14	63.6	4403765	3	Sequence 17119, A
C 13	14	63.6	4411529	3	Sequence 17119, A
C 14	13	59.1	240	4	US-09-103-840A-2
C 15	13	59.1	601	4	Sequence 216, App
C 16	13	59.1	601	4	Sequence 21714, A
C 17	13	59.1	601	4	Sequence 60781, A
C 18	13	59.1	601	4	Sequence 60782, A
C 19	13	59.1	601	4	Sequence 60783, A
C 20	13	59.1	1161	4	Sequence 164641, A
C 21	13	59.1	1411	4	Sequence 3861, Ap
C 22	13	59.1	1411	4	Sequence 505, App
C 23	13	59.1	1411	4	Sequence 4615, Ap
C 24	13	59.1	1546	4	Sequence 452, App
C 25	13	59.1	3250	3	Sequence 960, App
C 26	13	59.1	3935	3	Sequence 1, Appli
C 27	13	59.1	4082	4	Sequence 2722, Ap
C 28	13	59.1	4082	4	Sequence 50, Appli

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c 295 12 54.5 153866 4 US-09-949-016-16919 Sequence 16919, A
c 296 12 54.5 165651 4 US-09-949-016-13032 Sequence 13032, A
c 297 12 54.5 168971 4 US-09-949-016-13807 Sequence 13807, A
c 298 12 54.5 183202 4 US-09-949-016-13614 Sequence 13614, A
c 299 12 54.5 183770 4 US-09-949-016-15494 Sequence 15494, A
c 300 12 54.5 183770 4 US-09-949-016-15494 Sequence 15494, A

ALIGNMENTS

RESULT 1
US-09-949-016-16420/c
; Sequence 16420, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768

us-10-848-737-1.oli.rni
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16420
; LENGTH: 234884
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(234884)
; OTHER INFORMATION: n = A, T, C or G
US-09-949-016-16420
Query Match 68.2%; Score 15; DB 4; Length 234884;
Best Local Similarity 80.0%; Pred. No. 5.2;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 8 CACUCGUGAGCUCTT 22
||||:||||:||||
Db 140861 CACTCGTGAGCTCTT 140847

RESULT 2
US-09-134-001C-2127
; Sequence 2127, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 2127
; LENGTH: 348
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-2127
Query Match 63.6%; Score 14; DB 3; Length 348;
Best Local Similarity 71.4%; Pred. No. 26;
Matches 10; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 GUGAACUCACUCGU 14
||||:||||:||||
Db 134 GTGAAGTCACTCGT 147

RESULT 3
US-09-270-767-8994
; Sequence 8994, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8994
; LENGTH: 428
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-8994
```

Query Match 63.6%; Score 14; DB 4; Length 428;
Best Local Similarity 71.4%; Pred. No. 26;
Matches 10; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 7 UCACUCGUGAGCUC 20
Db 356 TCACGCTGAGCTC 369
:||||:|||||

RESULT 4

US-09-270-767-24276
; Sequence 24276, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Honburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24276
; LENGTH: 428
; TYPE: DNA
; ORGANISM: *Drosophila melanogaster*
US-09-270-767-24276

Query Match 63.6%; Score 14; DB 4; Length 428;
Best Local Similarity 71.4%; Pred. No. 26;
Matches 10; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 7 UCACUCGUGAGCUC 20
Db 356 TCACGCTGAGCTC 369
:||||:|||||

RESULT 5

US-09-710-279-3849
; Sequence 3849, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/09/710,279
; CURRENT FILING DATE: 2000-11-09
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3849
; LENGTH: 3170
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-09-710-279-3849

Query Match 63.6%; Score 14; DB 4; Length 3170;
Best Local Similarity 71.4%; Pred. No. 24;
Matches 10; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 GUGAACUCACUCGU 14
Db 1090 GTGAACCTCACTCGT 1103
|:||||:||||:

RESULT 6

US-09-710-279-2051
; Sequence 2051, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:

; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/09/710,279
; CURRENT FILING DATE: 2000-11-09
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2051
; LENGTH: 4329
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-09-710-279-2051

Query Match 63.6%; Score 14; DB 4; Length 4329;
Best Local Similarity 71.4%; Pred. No. 24;
Matches 10; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 GUGAACUCACUCGU 14
Db 101 GTGAACCTCACTCGT 114
|:||||:||||:

RESULT 7

US-09-949-016-11868/c
; Sequence 11868, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11868
; LENGTH: 300598
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(300598)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-11868

Query Match 63.6%; Score 14; DB 4; Length 300598;
Best Local Similarity 78.6%; Pred. No. 21;
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 9 ACUCGUGAGCUCTT 22
Db 93184 ACTCGTGAGCTCTT 93171
|:||||:||||:

RESULT 8

US-09-949-016-14588/c
; Sequence 14588, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14588
; LENGTH: 302604
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(302604)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14588

Query Match 63.6%; Score 14; DB 4; Length 302604;
Best Local Similarity 78.6%; Pred. No. 21;
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 9 ACUCUGAGCUCTT 22
||:|||||:
Db 143190 ACTCGTGAGCTCTT 143177

RESULT 9
US-09-949-016-14589/c
; Sequence 14589, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14589
; LENGTH: 302604
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(302604)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14589

Query Match 63.6%; Score 14; DB 4; Length 302604;
Best Local Similarity 78.6%; Pred. No. 21;
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 9 ACUCUGAGCUCTT 22
||:|||||:
Db 143190 ACTCGTGAGCTCTT 143177

RESULT 10
US-09-949-016-17119/c
; Sequence 17119, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17119
; LENGTH: 308362
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(308362)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17119

Query Match 63.6%; Score 14; DB 4; Length 308362;
Best Local Similarity 78.6%; Pred. No. 21;
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 9 ACUCUGAGCUCTT 22
||:|||||:
Db 143006 ACTCGTGAGCTCTT 142993

RESULT 11
US-09-103-840A-2/c
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentcin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match 63.6%; Score 14; DB 3; Length 4403765;
Best Local Similarity 71.4%; Pred. No. 18;
Matches 10; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CUCACUCUGAGCU 19
||:|||||:
Db 786568 CTCACGCGAGCT 786555

RESULT 12
US-09-103-840A-1/c
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:


```
; ORGANISM: Human
US-09-949-016-60782

Query Match          59.1%; Score 13; DB 4; Length 601;
Best Local Similarity 76.9%; Pred. No. 1e+02;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GUGAACUCACUCG 13
   |:|:|:|:|:|:|
Db 339 GTGAACCTCACTCG 327

RESULT 17
US-09-949-016-60783/c
; Sequence 60783, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60783
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-60783

Query Match          59.1%; Score 13; DB 4; Length 601;
Best Local Similarity 76.9%; Pred. No. 1e+02;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GUGAACUCACUCG 13
   |:|:|:|:|:|:|
Db 332 GTGAACCTCACTCG 320

RESULT 18
US-09-949-016-60784/c
; Sequence 60784, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60784
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-60784

Query Match          59.1%; Score 13; DB 4; Length 601;
Best Local Similarity 76.9%; Pred. No. 1e+02;
```

```
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GUGAACUCACUCG 13
   |:|:|:|:|:|:|
Db 233 GTGAACCTCACTCG 221

RESULT 19
US-09-949-016-164641
; Sequence 164641, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 164641
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-164641

Query Match          59.1%; Score 13; DB 4; Length 601;
Best Local Similarity 76.9%; Pred. No. 1e+02;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 4 AACUCACUCGUGA 16
   |:|:|:|:|:|:|
Db 238 AACCTCACTCGTGA 250

RESULT 20
US-09-543-681A-3861
; Sequence 3861, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 3861
; LENGTH: 1161
; TYPE: DNA
; ORGANISM: Proteus mirabilis
US-09-543-681A-3861

Query Match          59.1%; Score 13; DB 4; Length 1161;
Best Local Similarity 69.2%; Pred. No. 1e+02;
Matches 9; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 7 UCACUCGUGAGCU 19
   |:|:|:|:|:|:|
Db 170 TCACTCGTGAGCT 182

RESULT 21
US-09-949-016-505
; Sequence 505, Application US/09949016
```

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; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 505
; LENGTH: 1411
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-505

Query Match          59.1%; Score 13; DB 4; Length 1411;
Best Local Similarity 76.9%; Pred. No. 1e+02;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy      4 AACUCACUCGUGA 16
      |||:||||:||||
Db      453 AACTCACTCGTGA 465

RESULT 22
US-09-949-016-4615
; Sequence 4615, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4615
; LENGTH: 1411
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-4615

Query Match          59.1%; Score 13; DB 4; Length 1411;
Best Local Similarity 76.9%; Pred. No. 1e+02;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy      4 AACUCACUCGUGA 16
      |||:||||:||||
Db      453 AACTCACTCGTGA 465

RESULT 23
US-09-620-312D-452
; Sequence 452, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
```

```
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yunding
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghast
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6569662el Nucleic Acids and
; POLYPEPTIDES
; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/09/620,312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pt_FL_genes Version 1.0
; SEQ ID NO 452
; LENGTH: 1546
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (404)..(1189)
US-09-620-312D-452

Query Match          59.1%; Score 13; DB 4; Length 1546;
Best Local Similarity 76.9%; Pred. No. 99;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy      4 AACUCACUCGUGA 16
      |||:||||:||||
Db      572 AACTCACTCGTGA 584

RESULT 24
US-09-221-017B-960/c
; Sequence 960, Application US/09221017B
; Patent No. 6444799
; GENERAL INFORMATION:
; APPLICANT: Ross, Bruce C.
; TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
; NUMBER OF SEQUENCES: 1120
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/221,017B
; FILING DATE: 23-DEC-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PP1182
; FILING DATE: 31-DEC-1997
; PRIOR APPLICATION DATA: PP1546
; APPLICATION NUMBER: PP1546
; FILING DATE: 30-JAN-1998
```

;; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PP2911
; FILING DATE: 09-APR-1998
;; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/AU98/01023
; FILING DATE: 10-DEC-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Monroy, Gladys H
; REGISTRATION NUMBER: 32,430
; REFERENCE/DOCKET NUMBER: 27340-20021.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-813-5600
; TELEFAX: 650-494-0792
; TELEX: 706141
;; INFORMATION FOR SEQ ID NO: 960:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3250 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: UNKNOWN
; ORIGINAL SOURCE:
; ORGANISM: PORPHYROMONAS GINGIVALIS
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1...3250
US-09-221-017B-960

Query Match 59.1%; Score 13; DB 3; Length 3250;
Best Local Similarity 76.9%; Pred. No. 97;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GUGAACUCACUCG 13
|:|||||:|||||
Db 2826 GTGAACCTCACTCG 2814

RESULT 25
US-09-060-482-1/c
; Sequence 1, Application US/09060482
; Patent No. 6468766
; GENERAL INFORMATION:
; APPLICANT: Lee, Mu-En
; APPLICANT: Layne, Matthew D.
; APPLICANT: Yet, Shaw-Fang
; TITLE OF INVENTION: AORTIC CARDOXYPEPTIDASE-LIKE POLYPEPTIDE
; FILE REFERENCE: 05433/036001
; CURRENT APPLICATION NUMBER: US/09/060,482
; CURRENT FILING DATE: 1998-04-15
; EARLIER APPLICATION NUMBER: US 08/818,009
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: US 60/013,439
; EARLIER FILING DATE: 1996-03-15
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Fast-SEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 3935
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (140)...(3613)
US-09-060-482-1

Query Match 59.1%; Score 13; DB 3; Length 3935;
Best Local Similarity 76.9%; Pred. No. 96;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 10 CUCGUGAGCUCTT 22
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Db 1925 CTCGTGAGCTCTT 1913

RESULT 26

US-09-949-016-2722/c
; Sequence 2722, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 2722
; LENGTH: 4082
; TYPE: DNA
; ORGANISM: Human
; OTHER INFORMATION: pdv8 plasmid
US-09-949-016-2722

Query Match 59.1%; Score 13; DB 4; Length 4082;
Best Local Similarity 76.9%; Pred. No. 96;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 10 CUCGUGAGCUCTT 22
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Db 2092 CTCGTGAGCTCTT 2080

RESULT 27

US-09-525-305-50
; Sequence 50, Application US/09525305
; Patent No. 6806062
; GENERAL INFORMATION:
; APPLICANT: Hjort, Carsten
; APPLICANT: Hondel, C.A.M.J.J. van den
; APPLICANT: Punt, P.J.
; APPLICANT: Shuren, F.H.J.
; APPLICANT: Christensen, Tove
; TITLE OF INVENTION: Fungal Transcriptional Activator Useful in Methods For Producing
; Polypeptides
; FILE REFERENCE: 5555.400-US
; CURRENT APPLICATION NUMBER: US/09/525,305
; CURRENT FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 50
; LENGTH: 6015
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pdv8 plasmid
US-09-525-305-50

Query Match 59.1%; Score 13; DB 4; Length 6015;
Best Local Similarity 76.9%; Pred. No. 95;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 9 ACUCGUGAGCUCT 21
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Db 350 ACTCGTGAGCTCT 362

RESULT 28

US-09-949-016-12281
; Sequence 12281, Application US/09949016

; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12281
; LENGTH: 6831
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12281

Query Match 59.1%; Score 13; DB 4; Length 6831;
Best Local Similarity 69.2%; Pred. No. 95;
Matches 9; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 7 UCACUGUGAGCU 19
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Db 1201 TCACGCTGAGCT 1213

RESULT 29
US-09-949-016-14464/c
; Sequence 14464, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14464
; LENGTH: 14205
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14464

Query Match 59.1%; Score 13; DB 4; Length 14205;
Best Local Similarity 76.9%; Pred. No. 92;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 10 CUCGUGAGCUCTT 22
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Db 9218 CTCGTGAGCTCTT 9206

RESULT 30
US-09-949-016-12247
; Sequence 12247, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12247
; LENGTH: 14395
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12247

Query Match 59.1%; Score 13; DB 4; Length 14395;
Best Local Similarity 76.9%; Pred. No. 92;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 AACUCACUCUGGA 16
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Db 11437 AACCTCACTCGTGA 11449

Search completed: July 21, 2005, 00:58:19
Job time : 147 secs

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OM nucleic - nucleic search, using sw model

Run on: July 20, 2005, 23:27:36 ; Search time 605 Seconds
(without alignments)
230.700 Million cell updates/sec

Title: US-10-848-737-1

Perfect score: 22
Sequence: 1 gugaacucacugagacutt 22

Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 7173243 seqs, 3172129809 residues

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

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- 11: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
- 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
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- 19: /cgn2_6/ptodata/2/pubpna/US10G_PUBCOMB.seq.*
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- 21: /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq.*
- 22: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 23: /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq.*
- 24: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 25: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
- 26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	20	90.9	1215	21	US-10-831-901A-29766
5	20	90.9	1706	21	US-10-899-936-4
6	20	90.9	1706	21	US-10-899-936-14
7	20	90.9	24774	21	US-10-889-447-3

8	20	90.9	24774	21	US-10-831-901A-29748	Sequence 29748, A
9	20	90.9	24774	21	US-10-889-101-3	Sequence 3, Appli
10	20	90.9	28920	21	US-10-889-447-5	Sequence 5, Appli
11	20	90.9	28920	21	US-10-889-447-6	Sequence 6, Appli
12	20	90.9	28920	21	US-10-831-901A-29740	Sequence 29740, A
13	20	90.9	28920	21	US-10-889-101-5	Sequence 5, Appli
14	20	90.9	28920	21	US-10-889-101-6	Sequence 6, Appli
15	20	90.9	29013	21	US-10-831-901A-29819	Sequence 29819, A
16	20	90.9	29206	21	US-10-831-901A-29742	Sequence 29742, A
17	20	90.9	29291	21	US-10-889-447-4	Sequence 4, Appli
18	20	90.9	29291	21	US-10-831-901A-29738	Sequence 29738, A
19	20	90.9	29291	21	US-10-889-101-4	Sequence 4, Appli
20	20	90.9	29429	21	US-10-831-901A-29739	Sequence 29739, A
21	20	90.9	29430	21	US-10-889-447-7	Sequence 7, Appli
22	20	90.9	29430	21	US-10-831-901A-29741	Sequence 29741, A
23	20	90.9	29430	21	US-10-889-101-7	Sequence 7, Appli
24	20	90.9	29573	21	US-10-831-901A-29802	Sequence 29802, A
25	20	90.9	29573	21	US-10-831-901A-29803	Sequence 29803, A
26	20	90.9	29573	21	US-10-831-901A-29807	Sequence 29807, A
27	20	90.9	29592	21	US-10-831-901A-29820	Sequence 29820, A
28	20	90.9	29705	21	US-10-831-901A-29758	Sequence 29758, A
29	20	90.9	29705	21	US-10-831-901A-29791	Sequence 29791, A
30	20	90.9	29706	21	US-10-831-901A-29756	Sequence 29756, A
31	20	90.9	29706	21	US-10-831-901A-29793	Sequence 29793, A
32	20	90.9	29711	21	US-10-831-901A-29755	Sequence 29755, A
33	20	90.9	29711	21	US-10-831-901A-29757	Sequence 29757, A
34	20	90.9	29711	21	US-10-831-901A-29759	Sequence 29759, A
35	20	90.9	29711	21	US-10-831-901A-29799	Sequence 29799, A
36	20	90.9	29711	21	US-10-831-901A-29790	Sequence 29790, A
37	20	90.9	29711	21	US-10-831-901A-29792	Sequence 29792, A
38	20	90.9	29711	21	US-10-831-901A-29794	Sequence 29794, A
39	20	90.9	29715	21	US-10-831-901A-29815	Sequence 29815, A
40	20	90.9	29715	21	US-10-831-901A-29760	Sequence 29760, A
41	20	90.9	29715	21	US-10-831-901A-29795	Sequence 29795, A
42	20	90.9	29715	21	US-10-831-901A-29816	Sequence 29816, A
43	20	90.9	29720	21	US-10-831-901A-29798	Sequence 29798, A
44	20	90.9	29725	21	US-10-831-901A-29774	Sequence 29774, A
45	20	90.9	29725	21	US-10-831-901A-29781	Sequence 29781, A
46	20	90.9	29725	21	US-10-831-901A-29785	Sequence 29785, A
47	20	90.9	29727	21	US-10-839-729-15	Sequence 15, Appli
48	20	90.9	29727	21	US-10-827-757-1	Sequence 1, Appli
49	20	90.9	29727	21	US-10-889-447-8	Sequence 8, Appli
50	20	90.9	29727	21	US-10-699-936-1	Sequence 1, Appli
51	20	90.9	29727	21	US-10-831-901A-29737	Sequence 29737, A
52	20	90.9	29727	21	US-10-831-901A-29773	Sequence 29773, A
53	20	90.9	29727	21	US-10-831-901A-29780	Sequence 29780, A
54	20	90.9	29727	21	US-10-831-901A-29782	Sequence 29782, A
55	20	90.9	29727	21	US-10-831-901A-29783	Sequence 29783, A
56	20	90.9	29727	21	US-10-831-901A-29784	Sequence 29784, A
57	20	90.9	29727	21	US-10-831-901A-29812	Sequence 29812, A
58	20	90.9	29727	21	US-10-831-901A-29813	Sequence 29813, A
59	20	90.9	29727	21	US-10-831-901A-29822	Sequence 29822, A
60	20	90.9	29727	21	US-10-889-101-8	Sequence 8, Appli
61	20	90.9	29727	22	US-10-843-527-238196	Sequence 238196, A
62	20	90.9	29729	21	US-10-831-901A-29762	Sequence 29762, A
63	20	90.9	29729	21	US-10-831-901A-29771	Sequence 29771, A
64	20	90.9	29729	21	US-10-831-901A-29821	Sequence 29821, A
65	20	90.9	29729	21	US-10-831-901A-29823	Sequence 29823, A
66	20	90.9	29729	21	US-10-831-901A-29824	Sequence 29824, A
67	20	90.9	29729	21	US-10-831-901A-29825	Sequence 29825, A
68	20	90.9	29729	21	US-10-831-901A-29826	Sequence 29826, A
69	20	90.9	29729	21	US-10-831-901A-29827	Sequence 29827, A
70	20	90.9	29729	21	US-10-831-901A-29828	Sequence 29828, A
71	20	90.9	29729	21	US-10-831-901A-29829	Sequence 29829, A
72	20	90.9	29729	21	US-10-831-901A-29830	Sequence 29830, A
73	20	90.9	29731	21	US-10-831-901A-29797	Sequence 29797, A
74	20	90.9	29732	21	US-10-831-901A-29771	Sequence 29771, A
75	20	90.9	29732	21	US-10-831-901A-29788	Sequence 29788, A
76	20	90.9	29735	21	US-10-831-901A-29814	Sequence 29814, A
77	20	90.9	29736	21	US-10-839-729-17	Sequence 17, Appli
78	20	90.9	29736	21	US-10-889-447-9	Sequence 9, Appli
79	20	90.9	29736	21	US-10-699-936-3	Sequence 3, Appli
80	20	90.9	29736	21	US-10-831-901A-16	Sequence 16, Appli

81	20	90.9	29736	21	US-10-831-901A-29746	Sequence 29746, A		15	68.2	1870	9	US-09-864-761-21483	Sequence 21483, A
82	20	90.9	29736	21	US-10-831-901A-29747	Sequence 29747, A	c 154	15	68.2	1966	9	US-09-864-761-21483	Sequence 21483, A
83	20	90.9	29736	21	US-10-831-901A-29749	Sequence 29749, A	c 155	15	68.2	4317	19	US-10-755-889-778	Sequence 778, App
84	20	90.9	29736	21	US-10-831-901A-29750	Sequence 29750, A	c 157	15	68.2	5242	18	US-10-620-914-43	Sequence 43, Appl
85	20	90.9	29736	21	US-10-831-901A-29763	Sequence 29763, A	c 158	14	63.6	20	21	US-10-831-901A-774	Sequence 774, App
86	20	90.9	29736	21	US-10-831-901A-29769	Sequence 29769, A	c 159	14	63.6	20	21	US-10-831-901A-786	Sequence 786, App
87	20	90.9	29736	21	US-10-831-901A-29804	Sequence 29804, A	c 160	14	63.6	348	22	US-10-724-972A-609	Sequence 609, App
88	20	90.9	29736	21	US-10-831-901A-29805	Sequence 29805, A	c 161	14	63.6	535	13	US-10-027-633-187522	Sequence 187522, App
89	20	90.9	29736	21	US-10-831-901A-29806	Sequence 29806, A	c 162	14	63.6	535	17	US-10-027-633-187522	Sequence 187522, App
90	20	90.9	29736	21	US-10-889-101-9	Sequence 9806, A	c 163	14	63.6	579	18	US-10-424-593-86013	Sequence 86013, A
91	20	90.9	29736	22	US-10-843-527-238193	Sequence 238193, Appl	c 164	14	63.6	603	20	US-10-425-115-132098	Sequence 132098, A
92	20	90.9	29738	21	US-10-831-901A-29808	Sequence 29808, A	c 165	14	63.6	744	19	US-10-767-701-7756	Sequence 7756, App
93	20	90.9	29738	21	US-10-831-901A-29810	Sequence 29810, A	c 166	14	63.6	932	13	US-10-027-632-170009	Sequence 170009, App
94	20	90.9	29740	21	US-10-831-901A-29770	Sequence 29770, A	c 167	14	63.6	932	13	US-10-027-632-170011	Sequence 170011, App
95	20	90.9	29740	21	US-10-831-901A-29787	Sequence 29787, A	c 168	14	63.6	932	13	US-10-027-632-170011	Sequence 170011, App
96	20	90.9	29740	21	US-10-831-901A-29799	Sequence 29799, A	c 169	14	63.6	932	17	US-10-027-632-170009	Sequence 170009, App
97	20	90.9	29740	21	US-10-831-901A-29818	Sequence 29818, A	c 170	14	63.6	932	17	US-10-027-632-170010	Sequence 170010, App
98	20	90.9	29741	21	US-10-831-901A-29796	Sequence 29796, A	c 171	14	63.6	932	17	US-10-027-632-170011	Sequence 170011, App
99	20	90.9	29741	21	US-10-831-901A-29817	Sequence 29817, A	c 172	14	63.6	1278	17	US-10-369-493-43748	Sequence 43748, A
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102	20	90.9	29742	21	US-10-808-187-16	Sequence 16, Appl	c 175	14	63.6	3705	19	US-10-437-963-21697	Sequence 21697, A
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104	20	90.9	29742	21	US-10-808-187-737	Sequence 737, App	c 177	14	63.6	4704	19	US-10-437-963-21704	Sequence 21704, A
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c 108	20	90.9	29742	21	US-10-889-447-10	Sequence 10, Appl	c 181	14	63.6	7548	19	US-10-437-963-27706	Sequence 27706, A
109	20	90.9	29742	21	US-10-831-901A-29744	Sequence 14, Appl	c 182	14	63.6	8937	19	US-10-437-963-40275	Sequence 40275, A
110	20	90.9	29742	21	US-10-889-101-29	Sequence 10, Appl	c 183	14	63.6	47493	18	US-10-052-482-55	Sequence 55, Appl
111	20	90.9	29742	22	US-10-843-527-238194	Sequence 238194, Appl	c 184	14	63.6	76180	21	US-10-322-281-492	Sequence 492, App
112	20	90.9	29745	21	US-10-831-901A-29768	Sequence 29768, A	c 185	14	63.6	76698	21	US-10-936-273-30	Sequence 30, Appl
113	20	90.9	29745	21	US-10-831-901A-29811	Sequence 29811, A	c 186	14	63.6	76698	22	US-10-948-947A-1	Sequence 1, Appl
114	20	90.9	29749	21	US-10-831-901A-29809	Sequence 29809, A	c 187	14	63.6	110838	22	US-10-840-512-41	Sequence 41, Appl
115	20	90.9	29751	21	US-10-839-729-14	Sequence 14, Appl	c 188	14	63.6	247544	19	US-10-322-696-55	Sequence 55, Appl
116	20	90.9	29751	21	US-10-856-529-1	Sequence 1, Appl	c 189	13	59.1	20	21	US-10-831-901A-773	Sequence 773, App
117	20	90.9	29751	21	US-10-626-879-67	Sequence 67, Appl	c 190	13	59.1	20	21	US-10-831-901A-787	Sequence 787, App
118	20	90.9	29751	21	US-10-889-447-1	Sequence 1, Appl	c 191	13	59.1	21	17	US-09-842-758-110	Sequence 110, App
119	20	90.9	29751	21	US-10-889-447-2	Sequence 2, Appl	c 192	13	59.1	21	17	US-10-174-333-110	Sequence 110, App
120	20	90.9	29751	21	US-10-699-936-2	Sequence 2, Appl	c 193	13	59.1	21	17	US-10-174-333-186	Sequence 186, App
121	20	90.9	29751	21	US-10-831-901A-29751	Sequence 29751, A	c 194	13	59.1	22	18	US-10-335-977-9995	Sequence 9995, App
122	20	90.9	29751	21	US-10-831-901A-29752	Sequence 29752, A	c 195	13	59.1	25	22	US-10-719-956-73668	Sequence 73668, A
123	20	90.9	29751	21	US-10-831-901A-29778	Sequence 29778, A	c 196	13	59.1	25	22	US-10-719-956-78611	Sequence 78611, A
124	20	90.9	29751	21	US-10-831-901A-29801	Sequence 29801, A	c 197	13	59.1	25	22	US-10-719-956-308817	Sequence 308817, App
125	20	90.9	29751	21	US-10-889-101-1	Sequence 1, Appl	c 198	13	59.1	25	22	US-10-719-956-312434	Sequence 312434, App
126	20	90.9	29751	21	US-10-889-101-2	Sequence 2, Appl	c 199	13	59.1	25	22	US-10-719-956-501537	Sequence 501537, App
127	20	90.9	29751	22	US-10-843-527-238195	Sequence 238195, Appl	c 200	13	59.1	200	16	US-10-029-386-2454	Sequence 22454, A
128	20	90.9	29754	21	US-10-831-901A-29800	Sequence 29800, A	c 201	13	59.1	275	20	US-10-425-115-16480	Sequence 16480, A
129	20	90.9	29757	21	US-10-831-901A-29769	Sequence 29769, A	c 202	13	59.1	304	21	US-10-487-804-97	Sequence 97, Appl
130	20	90.9	29757	21	US-10-831-901A-29786	Sequence 29786, A	c 203	13	59.1	305	9	US-09-998-598-2109	Sequence 2109, App
131	20	90.9	29760	21	US-10-888-401-1	Sequence 1, Appl	c 204	13	59.1	314	20	US-10-425-115-33053	Sequence 33053, A
c 132	19	86.4	20	21	US-10-831-901A-779	Sequence 779, App	c 205	13	59.1	329	20	US-10-425-115-72056	Sequence 72056, A
c 133	19	86.4	20	21	US-10-831-901A-781	Sequence 781, App	c 206	13	59.1	382	20	US-10-425-115-145414	Sequence 145414, A
c 134	18	81.8	20	21	US-10-831-901A-778	Sequence 778, App	c 207	13	59.1	399	18	US-10-424-599-81718	Sequence 81718, A
c 135	18	81.8	20	21	US-10-831-901A-782	Sequence 782, App	c 208	13	59.1	399	20	US-10-425-115-168811	Sequence 168811, App
c 136	17	77.3	20	21	US-10-831-901A-777	Sequence 777, App	c 209	13	59.1	408	18	US-10-424-599-28283	Sequence 28283, A
c 137	17	77.3	20	21	US-10-831-901A-783	Sequence 783, App	c 210	13	59.1	413	11	US-09-732-627A-4252	Sequence 4252, App
c 138	16	72.7	20	21	US-10-831-901A-776	Sequence 776, App	c 211	13	59.1	420	17	US-10-242-535A-55663	Sequence 55663, A
c 139	16	72.7	20	21	US-10-831-901A-784	Sequence 784, App	c 212	13	59.1	420	18	US-10-085-783A-55663	Sequence 55663, A
c 140	16	72.7	619	21	US-10-487-901-5047	Sequence 5047, App	c 213	13	59.1	435	13	US-10-027-632-271544	Sequence 271544, App
141	16	72.7	619	21	US-10-487-901-5767	Sequence 5767, App	c 214	13	59.1	435	13	US-10-027-632-271544	Sequence 271544, App
142	16	72.7	686	21	US-10-487-901-1715	Sequence 1715, App	c 215	13	59.1	445	14	US-10-060-036-3310	Sequence 3310, App
143	16	72.7	686	21	US-10-487-901-5029	Sequence 5029, App	c 216	13	59.1	478	9	US-09-864-761-10972	Sequence 10972, A
144	16	72.7	1891	19	US-10-437-963-101306	Sequence 101306, Appl	c 217	13	59.1	486	10	US-09-918-995-7702	Sequence 7702, App
c 145	15	68.2	20	21	US-10-831-901A-775	Sequence 775, App	c 218	13	59.1	500	18	US-10-424-599-53113	Sequence 53113, A
c 146	15	68.2	20	21	US-10-831-901A-785	Sequence 785, App	c 219	13	59.1	506	13	US-10-027-632-315678	Sequence 315678, App
147	15	68.2	25	22	US-10-719-956-69911	Sequence 69911, A	c 220	13	59.1	506	17	US-10-027-632-315678	Sequence 315678, App
148	15	68.2	25	22	US-10-719-956-515621	Sequence 515621, A	c 221	13	59.1	520	13	US-10-027-632-212565	Sequence 212565, App
149	15	68.2	537	17	US-10-282-122A-38146	Sequence 38146, A	c 222	13	59.1	520	17	US-10-027-632-212565	Sequence 212565, App
c 150	15	68.2	627	14	US-10-000-256A-81	Sequence 81, Appl	c 223	13	59.1	545	13	US-10-027-632-6882	Sequence 6882, App
151	15	68.2	820	19	US-10-767-701-619	Sequence 619, App	c 224	13	59.1	545	13	US-10-027-632-6882	Sequence 6882, App
152	15	68.2	1101	19	US-10-767-793-2281	Sequence 2281, App	c 225	13	59.1	545	13	US-10-027-632-6882	Sequence 6882, App
c 153	15	68.2	1820	9	US-09-864-761-19662	Sequence 19662, A	c 226	13	59.1	545	17	US-10-027-632-6882	Sequence 6882, App

[illegible]

; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 780
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-780

Query Match 90.9%; Score 20; DB 21; Length 20;
Best Local Similarity 75.0%; Pred. No. 0.02;
Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 GUGAACUCACUCUGAGCUC 20
|:||||:||||:||||:|
Db 20 GTGAACCTCACTCGTGAGCTC 1

RESULT 3
US-10-755-415-166
; Sequence 166, Application US/10755415
; Publication No. US20050136480A1
; GENERAL INFORMATION:
; APPLICANT: BRAHMACHARI, SAMIR KUMAR
; APPLICANT: DASH, DEBASIS
; APPLICANT: SHARMA, RAMAKANT
; APPLICANT: MAHESHWARI, JITENDRA KUMAR
; TITLE OF INVENTION: A COMPUTER BASED VERSATILE METHOD FOR IDENTIFYING PROTEIN CODING
; FILE REFERENCE: 026033-00029
; CURRENT APPLICATION NUMBER: US/10755,415
; CURRENT FILING DATE: 2004-01-13
; PRIOR APPLICATION NUMBER: 10/727,989
; PRIOR FILING DATE: 2003-12-05
; NUMBER OF SEQ ID NOS: 373
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 166
; LENGTH: 525
; TYPE: DNA
; ORGANISM: Sars coronavirus
US-10-755-415-166

Query Match 90.9%; Score 20; DB 22; Length 525;
Best Local Similarity 75.0%; Pred. No. 0.014;
Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 GUGAACUCACUCUGAGCUC 20
|:||||:||||:||||:|
Db 76 GTGAACCTCACTCGTGAGCTC 95

RESULT 4
US-10-831-901A-29766
; Sequence 29766, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank

; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; FILE REFERENCE: ISIS0083-100 (BIOL00008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29766
; LENGTH: 1215
; TYPE: DNA
; ORGANISM: Sars Coronavirus
US-10-831-901A-29766

Query Match 90.9%; Score 20; DB 21; Length 1215;
Best Local Similarity 75.0%; Pred. No. 0.013;
Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 GUGAACUCACUCUGAGCUC 20
|:||||:||||:||||:|
Db 760 GTGAACCTCACTCGTGAGCTC 779

RESULT 5
US-10-699-936-4
; Sequence 4, Application US/10699936
; Publication No. US20050095582A1
; GENERAL INFORMATION:
; APPLICANT: Gillim-Ross, Laura
; APPLICANT: Taylor, Jill
; APPLICANT: Scholl, David R.
; APPLICANT: Wentworth, David E.
; APPLICANT: Jollick, Joseph D.
; TITLE OF INVENTION: Compositions and Methods for Detecting Severe Acute Respiratory
; FILE REFERENCE: DHI-07986
; CURRENT APPLICATION NUMBER: US/10/699,936
; CURRENT FILING DATE: 2003-11-03
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 1706
; TYPE: DNA
; ORGANISM: SARS-CoV Shanghai LY
US-10-699-936-4

Query Match 90.9%; Score 20; DB 21; Length 1706;
Best Local Similarity 75.0%; Pred. No. 0.012;
Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 GUGAACUCACUCUGAGCUC 20
|:||||:||||:||||:|
Db 697 GTGAACCTCACTCGTGAGCTC 716

RESULT 6
US-10-699-936-14
; Sequence 14, Application US/10699936
; Publication No. US20050095582A1
; GENERAL INFORMATION:
; APPLICANT: Gillim-Ross, Laura
; APPLICANT: Taylor, Jill


```

; APPLICANT: Scholl, David R.
; APPLICANT: Wentworth, David B.
; APPLICANT: Jollick, Joseph D.
; TITLE OF INVENTION: Compositions and Methods for Detecting Severe Acute Respiratory
; TITLE OF INVENTION: Syndrome Coronavirus
; FILE REFERENCE: DHI-07986
; CURRENT APPLICATION NUMBER: US/10/699,936
; CURRENT FILING DATE: 2003-11-03
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 1706
; TYPE: DNA
; ORGANISM: SARS coronavirus Shanghai LY
US-10-699-936-14

Query Match          90.9%; Score 20; DB 21; Length 1706;
Best Local Similarity 75.0%; Pred.No. 0.012; Indels 0; Gaps 0;
Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY      1  GUGAACUCACUCGUGAGCUC 20
        |:|:|:|:|:|:|:|:|:|:|
Db      697  GTGAACCTCACTCGTGAGCTC 716

RESULT 7
US-10-889-447-3
; Sequence 3, Application US/10889447
; Publication No. US20050075307A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; APPLICANT: Jain, Ravi
; TITLE OF INVENTION: MODULATION OF AMINOPEPTIDASE N EXPRESSION
; FILE REFERENCE: RTS-0685US
; CURRENT APPLICATION NUMBER: US/10/889,447
; CURRENT FILING DATE: 2004-07-12
; PRIOR APPLICATION NUMBER: 60/486,670
; PRIOR FILING DATE: 2003-07-12
; NUMBER OF SEQ ID NOS: 241
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 24774
; TYPE: DNA
; ORGANISM: SARS coronavirus isolate BJ01
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: n is any nucleotide
US-10-889-447-3

Query Match          90.9%; Score 20; DB 21; Length 24774;
Best Local Similarity 75.0%; Pred.No. 0.009; Indels 0; Gaps 0;
Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY      1  GUGAACUCACUCGUGAGCUC 20
        |:|:|:|:|:|:|:|:|:|:|
Db      706  GTGAACCTCACTCGTGAGCTC 725

RESULT 8
US-10-831-901A-29748
; Sequence 29748, Application US/10831901A
; Publication No. US20050100895A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian A.
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.

```

QY 1 GUGAACUCACUCGUGAGCUC 20
|:||||:||||:||||:|
Db 706 GTGAACCTCACTCGTGAGCTC 725

RESULT 10
US-10-889-447-5
; Sequence 5, Application US/10889447
; Publication No. US20050075307A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; APPLICANT: Jain, Ravi
; TITLE OF INVENTION: MODULATION OF AMINOPEPTIDASE N EXPRESSION
; FILE REFERENCE: RTS-0685US
; CURRENT APPLICATION NUMBER: US/10/889,447
; CURRENT FILING DATE: 2004-07-12
; PRIOR APPLICATION NUMBER: 60/486,670
; PRIOR FILING DATE: 2003-07-12
; NUMBER OF SEQ ID NOS: 241
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 28920
; TYPE: DNA
; ORGANISM: SARS coronavirus isolate BJ03
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: n is any nucleotide
US-10-889-447-5

Query Match 90.9%; Score 20; DB 21; Length 28920;
Best Local Similarity 75.0%; Pred. No. 0.0089;
Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 GUGAACUCACUCGUGAGCUC 20
|:||||:||||:||||:|
Db 776 GTGAACCTCACTCGTGAGCTC 795

RESULT 11
US-10-889-447-6
; Sequence 6, Application US/10889447
; Publication No. US20050075307A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; APPLICANT: Jain, Ravi
; TITLE OF INVENTION: MODULATION OF AMINOPEPTIDASE N EXPRESSION
; FILE REFERENCE: RTS-0685US
; CURRENT APPLICATION NUMBER: US/10/889,447
; CURRENT FILING DATE: 2004-07-12
; PRIOR APPLICATION NUMBER: 60/486,670
; PRIOR FILING DATE: 2003-07-12
; NUMBER OF SEQ ID NOS: 241
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 28920
; TYPE: DNA
; ORGANISM: SARS coronavirus isolate BJ04
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: n is any nucleotide
US-10-889-447-6

Query Match 90.9%; Score 20; DB 21; Length 28920;
Best Local Similarity 75.0%; Pred. No. 0.0089;
Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 GUGAACUCACUCGUGAGCUC 20
|:||||:||||:||||:|
Db 776 GTGAACCTCACTCGTGAGCTC 795

RESULT 12
US-10-831-901A-29740
; Sequence 29740, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swaze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; FILE REFERENCE: ISIS0083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29740
; LENGTH: 28920
; TYPE: DNA
; ORGANISM: SARS Coronavirus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 7230-7329, 9929-10028, 10137-10236, 11646-11745, 20385-20484,
; LOCATION: 21024-21123, 21753-21852, 22112-22211, 25301-25400
; OTHER INFORMATION: n = A,T,C or G
US-10-831-901A-29740

Query Match 90.9%; Score 20; DB 21; Length 28920;
Best Local Similarity 75.0%; Pred. No. 0.0089;
Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 GUGAACUCACUCGUGAGCUC 20
|:||||:||||:||||:|
Db 776 GTGAACCTCACTCGTGAGCTC 795

RESULT 13
US-10-889-101-5
; Sequence 5, Application US/10889101
; Publication No. US20050107324A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; APPLICANT: Dobie, Kenneth W.
; APPLICANT: Jain, Ravi
; TITLE OF INVENTION: MODULATION OF CEACAM1 EXPRESSION
; FILE REFERENCE: ISIS0101-100 (RTS-0655US)
; CURRENT APPLICATION NUMBER: US/10/889,101
; CURRENT FILING DATE: 2004-07-12
; PRIOR APPLICATION NUMBER: 60/486,652
; PRIOR FILING DATE: 2003-07-12
; NUMBER OF SEQ ID NOS: 298
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 28920
; TYPE: DNA

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; ORGANISM: SARS Coronavirus isolate BJ03
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: n = A,T,C or G
US-10-889-101-5

Query Match          90.9%; Score 20; DB 21; Length 28920;
Best Local Similarity 75.0%; Pred. No. 0.0089;
Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY      1  GUGAACUCACUCGUGAGCUC  20
Db      776  GTGAACCTCACTCGTGAGCTC  795
          |:||||:||||:||||:|

RESULT 14
US-10-889-101-6
; Sequence 6, Application US/10889101
; Publication No. US20050107324A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; APPLICANT: Dobie, Kenneth W.
; APPLICANT: Jain, Ravi
; TITLE OF INVENTION: MODULATION OF CEACAM1 EXPRESSION
; FILE REFERENCE: ISIS0101-100 (RTS-0655US)
; CURRENT APPLICATION NUMBER: US/10/889,101
; CURRENT FILING DATE: 2004-07-12
; PRIOR APPLICATION NUMBER: 60/486,652
; PRIOR FILING DATE: 2003-07-12
; NUMBER OF SEQ ID NOS: 298
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 28920
; TYPE: DNA
; ORGANISM: SARS Coronavirus isolate BJ04
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: n = A,T,C or G
US-10-889-101-6

Query Match          90.9%; Score 20; DB 21; Length 28920;
Best Local Similarity 75.0%; Pred. No. 0.0089;
Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY      1  GUGAACUCACUCGUGAGCUC  20
Db      776  GTGAACCTCACTCGTGAGCTC  795
          |:||||:||||:||||:|

RESULT 15
US-10-831-901A-29819
; Sequence 29819, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; FILE REFERENCE: ISIS0083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28

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Db      751 GTGAACTCACTCGTGAGCTC 770

RESULT 17
US-10-889-447-4
; Sequence 4, Application US/10889447
; Publication No. US20050075307A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; APPLICANT: Jain, Ravi
; TITLE OF INVENTION: MODULATION OF AMINOPEPTIDASE N EXPRESSION
; FILE REFERENCE: RTS-0685US
; CURRENT APPLICATION NUMBER: US/10/889,447
; CURRENT FILING DATE: 2004-07-12
; PRIOR APPLICATION NUMBER: 60/486,670
; PRIOR FILING DATE: 2003-07-12
; NUMBER OF SEQ ID NOS: 241
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 29291
; TYPE: DNA
; ORGANISM: SARS coronavirus isolate BJ02
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: n is any nucleotide
US-10-889-447-4

Query Match          90.9%; Score 20; DB 21; Length 29291;
Best Local Similarity 75.0%; Pred. No. 0.0089;
Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY      1 GUGAACUCACUCUGAGCUC 20
       |:||||:||||:||||:|
Db      726 GTGAACTCACTCGTGAGCTC 745

RESULT 18
US-10-831-901A-29738
; Sequence 29738, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian A.
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; TITLE OF INVENTION: Acute Respiratory Syndrome (SARS)
; FILE REFERENCE: ISIS0083-100 (BIOL00080US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29738
; LENGTH: 29291
; TYPE: DNA
; ORGANISM: SARS Coronavirus isolate BJ02
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: n = A,T,C or G
US-10-889-101-4

Query Match          90.9%; Score 20; DB 21; Length 29291;
Best Local Similarity 75.0%; Pred. No. 0.0089;
Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY      1 GUGAACUCACUCUGAGCUC 20
       |:||||:||||:||||:|
Db      726 GTGAACTCACTCGTGAGCTC 745

RESULT 19
US-10-889-101-4
; Sequence 4, Application US/10889101
; Publication No. US20050107324A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; APPLICANT: Dobie, Kenneth W.
; APPLICANT: Jain, Ravi
; TITLE OF INVENTION: MODULATION OF CEACAM1 EXPRESSION
; FILE REFERENCE: ISIS0101-100 (RTS-0655US)
; CURRENT APPLICATION NUMBER: US/10/889,101
; CURRENT FILING DATE: 2004-07-12
; PRIOR APPLICATION NUMBER: 60/486,652
; PRIOR FILING DATE: 2003-07-12
; NUMBER OF SEQ ID NOS: 298
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 29291
; TYPE: DNA
; ORGANISM: SARS Coronavirus isolate BJ02
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: n = A,T,C or G
US-10-889-101-4

Query Match          90.9%; Score 20; DB 21; Length 29291;
Best Local Similarity 75.0%; Pred. No. 0.0089;
Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY      1 GUGAACUCACUCUGAGCUC 20
       |:||||:||||:||||:|
Db      726 GTGAACTCACTCGTGAGCTC 745

RESULT 20
US-10-831-901A-29739
; Sequence 29739, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian A.
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; TITLE OF INVENTION: Acute Respiratory Syndrome (SARS)
; FILE REFERENCE: ISIS0083-100 (BIOL00080US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29738
; LENGTH: 29291
; TYPE: DNA
; ORGANISM: SARS Coronavirus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: n = A,T,C or G
US-10-831-901A-29738

Query Match          90.9%; Score 20; DB 21; Length 29291;
Best Local Similarity 75.0%; Pred. No. 0.0089;
Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY      1 GUGAACUCACUCUGAGCUC 20
       |:||||:||||:||||:|
Db      726 GTGAACTCACTCGTGAGCTC 745

RESULT 21
US-10-831-901A-29738
; Sequence 29738, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian A.
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; TITLE OF INVENTION: Acute Respiratory Syndrome (SARS)
; FILE REFERENCE: ISIS0083-100 (BIOL00080US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29738
; LENGTH: 29291
; TYPE: DNA
; ORGANISM: SARS Coronavirus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: n = A,T,C or G
US-10-831-901A-29738

Query Match          90.9%; Score 20; DB 21; Length 29291;
Best Local Similarity 75.0%; Pred. No. 0.0089;
Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY      1 GUGAACUCACUCUGAGCUC 20
       |:||||:||||:||||:|
Db      726 GTGAACTCACTCGTGAGCTC 745

RESULT 22
US-10-831-901A-29738
; Sequence 29738, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian A.
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; TITLE OF INVENTION: Acute Respiratory Syndrome (SARS)
; FILE REFERENCE: ISIS0083-100 (BIOL00080US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29738
; LENGTH: 29291
; TYPE: DNA
; ORGANISM: SARS Coronavirus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: n = A,T,C or G
US-10-831-901A-29738

Query Match          90.9%; Score 20; DB 21; Length 29291;
Best Local Similarity 75.0%; Pred. No. 0.0089;
Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY      1 GUGAACUCACUCUGAGCUC 20
       |:||||:||||:||||:|
Db      726 GTGAACTCACTCGTGAGCTC 745

RESULT 23
US-10-831-901A-29738
; Sequence 29738, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian A.
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
```

;; PRIOR APPLICATION NUMBER: 60/466,426
;; PRIOR FILING DATE: 2003-04-28
;; PRIOR APPLICATION NUMBER: 60/468,562
;; PRIOR FILING DATE: 2003-05-06
;; PRIOR APPLICATION NUMBER: 60/467,770
;; PRIOR FILING DATE: 2003-04-30
;; PRIOR APPLICATION NUMBER: 60/468,627
;; PRIOR FILING DATE: 2003-05-06
;; PRIOR APPLICATION NUMBER: 60/477,637
;; PRIOR FILING DATE: 2003-06-10
;; PRIOR APPLICATION NUMBER: 60/483,579
;; PRIOR FILING DATE: 2003-06-27
;; NUMBER OF SEQ ID NOS: 30063
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 29739
;; LENGTH: 29429
;; TYPE: DNA
;; ORGANISM: SARS Coronavirus
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: 860-959, 2509-2608, 3338-3437, 5551, 5767-5866, 7296-7395, 8908,
;; LOCATION: 10914-11014, 11744-11843, 14993-15092, 20606, 20953, 21432-21531,
;; LOCATION: 25728, 25746, 26631-26730, 28364
;; OTHER INFORMATION: n = A,T,C or G
US-10-831-901A-29739

Query Match 90.9%; Score 20; DB 21; Length 29429;
Best Local Similarity 75.0%; Pred. No. 0.0089;
Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GUGAACUCACUCGUGAGCUC 20
|:||||:||||:||||:|
Db 793 GTGAACCTCACTCGTGAGCTC 812

RESULT 21

US-10-889-447-7
;; Sequence 7, Application US/10889447
;; Publication No. US20050075307A1
;; GENERAL INFORMATION:
;; APPLICANT: Bennett, C. Frank
;; APPLICANT: Jain, Ravi
;; TITLE OF INVENTION: MODULATION OF AMINOPEPTIDASE N EXPRESSION
;; FILE REFERENCE: RTS-0685US
;; CURRENT APPLICATION NUMBER: US/10/889,447
;; CURRENT FILING DATE: 2004-07-12
;; PRIOR APPLICATION NUMBER: 60/486,670
;; PRIOR FILING DATE: 2003-07-12
;; NUMBER OF SEQ ID NOS: 241
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 7
;; LENGTH: 29430
;; TYPE: DNA
;; ORGANISM: SARS coronavirus isolate GZ01
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION:
;; OTHER INFORMATION: n is any nucleotide
US-10-889-447-7

Query Match 90.9%; Score 20; DB 21; Length 29430;
Best Local Similarity 75.0%; Pred. No. 0.0089;
Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GUGAACUCACUCGUGAGCUC 20
|:||||:||||:||||:|
Db 760 GTGAACCTCACTCGTGAGCTC 779

RESULT 22

US-10-831-901A-29741
;; Sequence 29741, Application US/10831901A
;; Publication No. US20050100885A1

;; GENERAL INFORMATION:
;; APPLICANT: Crooke, Stanley T.
;; APPLICANT: Ecker, David J.
;; APPLICANT: Sampath, Rangarajan
;; APPLICANT: Freier, Susan M.
;; APPLICANT: Massire, Christian
;; APPLICANT: Hofstadler, Steven A.
;; APPLICANT: Lowery, Kristin Sannes
;; APPLICANT: Swayze, Eric
;; APPLICANT: Baker, Brenda F.
;; APPLICANT: Bennett, C. Frank
;; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
;; TITLE OF INVENTION: Acute Respiratory Syndrome (SARS)
;; FILE REFERENCE: ISIS0083-100 (BIOL000808US)
;; CURRENT APPLICATION NUMBER: US/10/831,901A
;; CURRENT FILING DATE: 2004-04-26
;; PRIOR APPLICATION NUMBER: 60/466,426
;; PRIOR FILING DATE: 2003-04-28
;; PRIOR APPLICATION NUMBER: 60/468,562
;; PRIOR FILING DATE: 2003-05-06
;; PRIOR APPLICATION NUMBER: 60/467,770
;; PRIOR FILING DATE: 2003-04-30
;; PRIOR APPLICATION NUMBER: 60/468,627
;; PRIOR FILING DATE: 2003-05-06
;; PRIOR APPLICATION NUMBER: 60/477,637
;; PRIOR FILING DATE: 2003-06-10
;; PRIOR APPLICATION NUMBER: 60/483,579
;; PRIOR FILING DATE: 2003-06-27
;; NUMBER OF SEQ ID NOS: 30063
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 29741
;; LENGTH: 29430
;; TYPE: DNA
;; ORGANISM: SARS Coronavirus
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: 6464-6563, 11343-11442, 22567-22666
;; OTHER INFORMATION: n = A,T,C or G
US-10-831-901A-29741

Query Match 90.9%; Score 20; DB 21; Length 29430;
Best Local Similarity 75.0%; Pred. No. 0.0089;
Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GUGAACUCACUCGUGAGCUC 20
|:||||:||||:||||:|
Db 760 GTGAACCTCACTCGTGAGCTC 779

RESULT 23

US-10-889-101-7
;; Sequence 7, Application US/10889101
;; Publication No. US20050107324A1
;; GENERAL INFORMATION:
;; APPLICANT: Bennett, C. Frank
;; APPLICANT: Dobie, Kenneth W.
;; APPLICANT: Jain, Ravi
;; TITLE OF INVENTION: MODULATION OF CEACAM1 EXPRESSION
;; FILE REFERENCE: ISIS0101-100 (RTS-0655US)
;; CURRENT APPLICATION NUMBER: US/10/889,101
;; CURRENT FILING DATE: 2004-07-12
;; PRIOR APPLICATION NUMBER: 60/486,652
;; PRIOR FILING DATE: 2003-07-12
;; NUMBER OF SEQ ID NOS: 298
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 7
;; LENGTH: 29430
;; TYPE: DNA
;; ORGANISM: SARS Coronavirus isolate GZ01
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION:
;; OTHER INFORMATION: n = A,T,C or G

US-10-889-101-7

Query Match 90.9%; Score 20; DB 21; Length 29430;
Best Local Similarity 75.0%; Pred. No. 0.0089;
Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 GUGAACUCACUCUGAGCUC 20
|:||||:||||:||||:|
Db 760 GTGAACCTCACTCGTGAGCTC 779

RESULT 24

US-10-831-901A-29802
; Sequence 29802, Application US/10831901A
; Publication No. US20050100885A1

; GENERAL INFORMATION:

; APPLICANT: Crooke, Stanley T.

; APPLICANT: Ecker, David J.

; APPLICANT: Sampath, Rangarajan

; APPLICANT: Freier, Susan M.

; APPLICANT: Massire, Christian

; APPLICANT: Hofstadler, Steven A.

; APPLICANT: Lowery, Kristin Sannes

; APPLICANT: Swayze, Eric

; APPLICANT: Baker, Brenda F.

; APPLICANT: Bennett, C. Frank

; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe

; FILE REFERENCE: ISIS0083-100 (BIOL00008US)

; CURRENT APPLICATION NUMBER: US/10/831,901A

; CURRENT FILING DATE: 2004-04-26

; PRIOR APPLICATION NUMBER: 60/466,426

; PRIOR FILING DATE: 2003-04-28

; PRIOR APPLICATION NUMBER: 60/468,562

; PRIOR FILING DATE: 2003-05-06

; PRIOR APPLICATION NUMBER: 60/467,770

; PRIOR FILING DATE: 2003-04-30

; PRIOR APPLICATION NUMBER: 60/468,627

; PRIOR FILING DATE: 2003-05-06

; PRIOR APPLICATION NUMBER: 60/477,637

; PRIOR FILING DATE: 2003-06-10

; PRIOR APPLICATION NUMBER: 60/483,579

; NUMBER OF SEQ ID NOS: 30063

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 29802

; LENGTH: 29573

; TYPE: DNA

; ORGANISM: SARS Coronavirus

US-10-831-901A-29802

Query Match 90.9%; Score 20; DB 21; Length 29573;
Best Local Similarity 75.0%; Pred. No. 0.0089;
Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 GUGAACUCACUCUGAGCUC 20
|:||||:||||:||||:|
Db 707 GTGAACCTCACTCGTGAGCTC 726

RESULT 25

US-10-831-901A-29803

; Sequence 29803, Application US/10831901A

; Publication No. US20050100885A1

; GENERAL INFORMATION:

; APPLICANT: Crooke, Stanley T.

; APPLICANT: Ecker, David J.

; APPLICANT: Sampath, Rangarajan

; APPLICANT: Freier, Susan M.

; APPLICANT: Massire, Christian

; APPLICANT: Hofstadler, Steven A.

; APPLICANT: Lowery, Kristin Sannes

; APPLICANT: Swayze, Eric

; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; FILE REFERENCE: ISIS0083-100 (BIOL00008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29803
; LENGTH: 29573
; TYPE: DNA
; ORGANISM: SARS Coronavirus
US-10-831-901A-29803

Query Match 90.9%; Score 20; DB 21; Length 29573;
Best Local Similarity 75.0%; Pred. No. 0.0089;
Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 GUGAACUCACUCUGAGCUC 20
|:||||:||||:||||:|
Db 707 GTGAACCTCACTCGTGAGCTC 726

RESULT 26

US-10-831-901A-29807

; Sequence 29807, Application US/10831901A

; Publication No. US20050100885A1

; GENERAL INFORMATION:

; APPLICANT: Crooke, Stanley T.

; APPLICANT: Ecker, David J.

; APPLICANT: Sampath, Rangarajan

; APPLICANT: Freier, Susan M.

; APPLICANT: Massire, Christian

; APPLICANT: Hofstadler, Steven A.

; APPLICANT: Lowery, Kristin Sannes

; APPLICANT: Swayze, Eric

; APPLICANT: Baker, Brenda F.

; APPLICANT: Bennett, C. Frank

; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe

; FILE REFERENCE: ISIS0083-100 (BIOL00008US)

; CURRENT APPLICATION NUMBER: US/10/831,901A

; CURRENT FILING DATE: 2004-04-26

; PRIOR APPLICATION NUMBER: 60/466,426

; PRIOR FILING DATE: 2003-04-28

; PRIOR APPLICATION NUMBER: 60/468,562

; PRIOR FILING DATE: 2003-05-06

; PRIOR APPLICATION NUMBER: 60/467,770

; PRIOR FILING DATE: 2003-04-30

; PRIOR APPLICATION NUMBER: 60/468,627

; PRIOR FILING DATE: 2003-05-06

; PRIOR APPLICATION NUMBER: 60/477,637

; PRIOR FILING DATE: 2003-06-10

; PRIOR APPLICATION NUMBER: 60/483,579

; NUMBER OF SEQ ID NOS: 30063

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 29807

; LENGTH: 29573

; TYPE: DNA

```

; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; TITLE OF INVENTION: Acute Respiratory Syndrome (SARS)
; FILE REFERENCE: ISI90083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29758
; LENGTH: 29705
; TYPE: DNA
; ORGANISM: SARS Coronavirus
US-10-831-901A-29758

Query Match          90.9%; Score 20; DB 21; Length 29705;
Best Local Similarity 75.0%; Pred.No. 0.0089;
Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY      1   GUGAACUCACUCGUGAGCUC 20
        |:|::|::|::|::|::|::|:
Db       760 GTGAACCTCACTCGTGAGCTC 779

RESULT 29
US-10-831-901A-29791
; Sequence 29791, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; TITLE OF INVENTION: Acute Respiratory Syndrome (SARS)
; FILE REFERENCE: ISI90083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29791
; LENGTH: 29705

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; TYPE: DNA
; ORGANISM: SARS Coronavirus
US-10-831-901A-29791

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Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY      1 GUGAACUCACUCGUGAGCUC 20
Db      760 GTGAACCTCACTCGTGAGCTC 779

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; Sequence 29756, Application US/10831901A
; Publication No. US20050100895A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; TITLE OF INVENTION: Acute Respiratory Syndrome (SARS)
; FILE REFERENCE: ISIS0083-100 (BIOL00008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
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; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29756
; LENGTH: 29706
; TYPE: DNA
; ORGANISM: SARS Coronavirus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 20688
; OTHER INFORMATION: n = A,T,C or G
US-10-831-901A-29756

Query Match          90.9%; Score 20; DB 21; Length 29706;
Best Local Similarity 75.0%; Pred. No. 0.0089;
Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY      1 GUGAACUCACUCGUGAGCUC 20
Db      760 GTGAACCTCACTCGTGAGCTC 779

Search completed: July 21, 2005, 01:08:21
Job time : 609 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 20, 2005, 18:32:31 ; Search time 1685 Seconds
(without alignments)
632.650 Million cell updates/sec

Title: US-10-848-737-1

Perfect score: 22

Sequence: 1 gugaacucacugagucctt 22

Scoring table:

OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 4708233 seqs, 24227607955 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 300 summaries

Database :

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2: gb_hlg.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
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9: gb_pr.*
10: gb_ro.*
11: gb_Ste.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	20	90.9	29350	14	AY395000
7	20	90.9	29350	14	AY395001
8	20	90.9	29350	14	AY395002
9	20	90.9	29433	14	AY394977
10	20	90.9	29530	14	AY394985
11	20	90.9	29573	14	AY338174
12	20	90.9	29573	14	AY338175
13	20	90.9	29573	14	AY348314
14	20	90.9	29577	14	AY559094
15	20	90.9	29592	14	AY463059
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17	20	90.9	29640	14	AY394978
18	20	90.9	29645	14	AY394979
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94	20	90.9	29738	14	AY357075	AY357075 SARS coro	167	15	68.2	43599	9	HSU15177	U15177 Human cosmi
95	20	90.9	29740	14	AY278490	AY278490 SARS coro	168	15	68.2	50389	1	AE014137	AE014137 Streptoco
96	20	90.9	29740	14	AY310120	AY310120 SARS coro	C 169	15	68.2	51430	2	AC017981	AC017981 Drosophil
97	20	90.9	29740	14	AY485278	AY485278 SARS coro	C 170	15	68.2	54668	6	AX602203	AX602203 Sequence
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109	20	90.9	29760	14	AY390556	AY390556 SARS coro	182	15	68.2	157165	4	AC087843	AC087843 Bos tauru
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113	17	77.3	147433	2	AC137257	AC137257 Rattus no	186	15	68.2	162109	5	BX001032	BX001032 Zebrafish
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116	16	72.7	838	8	AK062203	AK062203 Oryza sat	C 189	15	68.2	164000	9	AL591682	AL591682 Human DNA
117	16	72.7	947	8	AK099574	AK099574 Oryza sat	C 190	15	68.2	164766	10	AC144792	AC144792 Mus muscu
118	16	72.7	120551	9	AL391215	AL391215 Human DNA	C 191	15	68.2	174839	9	AL157395	AL157395 Human DNA
C 119	16	72.7	127267	8	CNS0984U	EX119951 Oryza sat	C 192	15	68.2	184783	8	AC136972	AC136972 Oryza sat
120	16	72.7	138563	2	AC150484	AC150484 Bos tauru	C 193	15	68.2	188901	2	AC132886	AC132886 Mus muscu
121	16	72.7	176629	2	AC055792	AC055792 Homo sapi	194	15	68.2	189318	2	CR376821	CR376821 Danio rer
122	16	72.7	218200	2	AC141165	AC141165 Rattus no	195	15	68.2	189757	3	AC008186	AC008186 Drosophil
123	16	72.7	227026	2	AC136659	AC136659 Rattus no	C 196	15	68.2	190708	9	AC005261	AC005261 Homo sapi
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C 133	15	68.2	1820	6	CQ057040	CQ057040 Sequence	C 206	15	68.2	221753	2	AC114835	AC114835 Rattus no
C 134	15	68.2	1820	6	CQ076301	CQ076301 Sequence	207	15	68.2	227774	2	AC123156	AC123156 Rattus no
C 135	15	68.2	1820	6	CQ107294	CQ107294 Sequence	C 208	15	68.2	229061	9	AC007786	AC007786 Homo sapi
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C 139	15	68.2	1820	6	CQ304315	CQ304315 Sequence	C 212	15	68.2	234017	2	AC126997	AC126997 Rattus no
C 140	15	68.2	1820	6	CQ341583	CQ341583 Sequence	C 213	15	68.2	235382	2	AC130104	AC130104 Rattus no
C 141	15	68.2	1870	6	CQ078257	CQ078257 Sequence	214	15	68.2	243313	3	AE003834	AE003834 Drosophil
C 142	15	68.2	1870	6	CQ109247	CQ109247 Sequence	215	15	68.2	245066	2	AC094644	AC094644 Rattus no
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C 146	15	68.2	1870	6	CQ269291	CQ269291 Sequence	C 219	15	68.2	261031	2	AC140768	AC140768 Rattus no
C 147	15	68.2	1870	6	CQ306316	CQ306316 Sequence	C 220	15	68.2	270221	2	AC107500	AC107500 Rattus no
C 148	15	68.2	1870	6	CQ343438	CQ343438 Sequence	C 221	15	68.2	272796	2	AC133856	AC133856 Rattus no
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C 151	15	68.2	1966	6	CQ094118	CQ094118 Sequence	224	14	63.6	428	6	AR519316	AR519316 Sequence
C 152	15	68.2	1966	6	CQ171485	CQ171485 Sequence	C 225	14	63.6	488	12	AY200782	AY200782 Arabidops
C 153	15	68.2	1966	6	CQ200599	CQ200599 Sequence	C 226	14	63.6	534	6	CQ649386	CQ649386 Sequence
C 154	15	68.2	1966	6	CQ254675	CQ254675 Sequence	C 227	14	63.6	590	11	HS635N10S	AL031544 H. sapiens
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C 160	15	68.2	4089	6	CQ576314	CQ576314 Sequence	C 233	14	63.6	1341	6	AX061735	AX061735 Sequence
C 161	15	68.2	4317	9	HS276316	AJ276316 Homo sapi	C 234	14	63.6	1341	8	AF058905	AF058905 Oryza sat
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C 163	15	68.2	11518	10	MMU511265	AJ511265 Mus muscu	C 236	14	63.6	1497	3	AF083644	AF083644 Caenorhab
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ALIGNMENTS

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LOCUS SARS coronavirus Shanghai LY orfiab polyprotein and orfiA
DEFINITION SARS coronavirus genes, partial cds.
ACCESSION AY322205

VERSION AY322205.1 GI:32454339
KEYWORDS 1 of 4
SEGMENT SARS coronavirus Shanghai LY
ORGANISM SARS coronavirus Shanghai LY
Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.
REFERENCE 1 (bases 1 to 1706)
Yuan, Z., Zhang, X., Hu, Y., Lan, S., Wang, H., Zhou, Z. and Wen, Y.
Submitted (12-JUN-2003) Molecular Virology, Shanghai Medical
College of Fudan University, 138 Yi Xue Yuan Road, Shanghai 200032,
P.R. China
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DEFINITION	AY394999	
ACCESSION	AY394999.1 GI:37624342	
VERSION		
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SOURCE	SARS coronavirus LC2	
ORGANISM	Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales; Coronaviridae; Coronavirus.	
REFERENCE	1 (bases 1 to 29350)	
AUTHORS	The SARS epidemiology consortium of Guangdong	
CONSTRM	From independent foci of epidemic outbreak to large genomic alteration in late phase viruses: evolution of the SARS-coronavirus	
TITLE	Unpublished	
JOURNAL	2 (bases 1 to 29350)	
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AUTHORS	The SARS epidemiology consortium of Guangdong	
CONSTRM	Direct Submission	
TITLE	Submitted (19-SEP-2003) Guangdong, China	
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DEFINITION	AY395000	
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VERSION		
KEYWORDS	SARS coronavirus LC3	
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REFERENCE	1 (bases 1 to 29350)	
AUTHORS	The SARS epidemiology consortium of Guangdong	
CONSTRM	From independent foci of epidemic outbreak to large genomic alteration in late phase viruses: evolution of the SARS-coronavirus	
TITLE	Unpublished	
JOURNAL	2 (bases 1 to 29350)	
REFERENCE		
AUTHORS		


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TITLE      From independent foci of epidemic outbreak to large genomic
JOURNAL    alteration in late phase viruses: evolution of the SARS-coronavirus
REFERENCE  2 (bases 1 to 29350)
AUTHORS    The SARS epidemiology consortium of Guangdong
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DEFINITION SARS coronavirus GZ-A, partial genome.
ACCESSION  AY394977
VERSION    AY394977.1 GI:37624320
KEYWORDS
SOURCE    SARS coronavirus GZ-A
ORGANISM  SARS coronavirus GZ-A
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REFERENCE  1 (bases 1 to 29433)
AUTHORS    The SARS epidemiology consortium of Guangdong
CONSTRM    From independent foci of epidemic outbreak to large genomic
TITLE      alteration in late phase viruses: evolution of the SARS-coronavirus
JOURNAL    Unpublished
REFERENCE  2 (bases 1 to 29433)
AUTHORS    The SARS epidemiology consortium of Guangdong
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TITLE      Submitted (19-SEP-2003) Guangdong, China
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RESULT 10
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LOCUS      AY394985      29530 bp      RNA      linear      VRL 29-JAN-2004
DEFINITION SARS coronavirus HSZ-Bb, complete genome.
ACCESSION  AY394985
VERSION    AY394985.1 GI:37624328
KEYWORDS
SOURCE    SARS coronavirus HSZ-Bb
ORGANISM  SARS coronavirus HSZ-Bb

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Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
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REFERENCE  1 (bases 1 to 29530)
AUTHORS    The SARS epidemiology consortium of Guangdong
CONSTRM    From independent foci of epidemic outbreak to large genomic
TITLE      alteration in late phase viruses: evolution of the SARS-coronavirus
JOURNAL    Unpublished
REFERENCE  2 (bases 1 to 29530)
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RESULT 11
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DEFINITION SARS coronavirus Taiwan TC1, complete genome.
ACCESSION  AY338174
VERSION    AY338174.1 GI:32493129
KEYWORDS
SOURCE    SARS coronavirus Taiwan TC1
ORGANISM  SARS coronavirus Taiwan TC1
           Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
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REFERENCE  1 (bases 1 to 29573)
AUTHORS    Chang,J.-G.C., Lin,T.-H., Chen,C.-M., Lin,C.-S., Chan,W.-L. and
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TITLE      SARS coronavirus TC1, clinical specimen
JOURNAL    Unpublished
REFERENCE  2 (bases 1 to 29573)
AUTHORS    Chang,J.-G.C., Lin,T.-H., Chen,C.-M., Lin,C.-S., Chan,W.-L. and
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TITLE      Direct Submission
JOURNAL    Submitted (08-JUL-2003) Department of Molecular Medicine, China
           Medical University Hospital, 2, Yuh Der Road, Taichung, Taichung
           404, Taiwan
REFERENCE  3 (bases 1 to 29573)
AUTHORS    Chang,J.-G.C., Lin,T.-H., Chen,C.-M., Lin,C.-S., Chan,W.-L. and
           Shih,M.-C.
TITLE      Direct Submission
JOURNAL    Submitted (28-JUL-2003) Department of Molecular Medicine, China
           Medical University Hospital, 2, Yuh Der Road, Taichung, Taichung
           404, Taiwan
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REFERENCE 1 (bases 1 to 29573)
AUTHORS Chang, J., Lin, T., Chen, C., Lin, T., Chan, W. and Shih, M.
TITLE SARS coronavirus TC2, clinical specimen
JOURNAL Unpublished
2 (bases 1 to 29573)
AUTHORS Chang, J., Lin, T., Chen, C., Lin, T., Chan, W. and Shih, M.
TITLE Direct Submission
JOURNAL Submitted (09-JUL-2003) Department of Molecular Medicine, China Medical University Hospital, 2, Yuh Der Road, Taichung, Taichung 404, Taiwan

REFERENCE 3 (bases 1 to 29573)
AUTHORS Chang, J., Lin, T., Chen, C., Lin, T., Chan, W. and Shih, M.
TITLE Direct Submission
JOURNAL Submitted (28-JUL-2003) Department of Molecular Medicine, China Medical University Hospital, 2, Yuh Der Road, Taichung, Taichung 404, Taiwan

REMARK Amino acid sequence updated by submitter
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CPDS

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              The SARS epidemiology consortium of Guangdong
              From independent foci of epidemic outbreak to large genomic
              alteration in late phase viruses: evolution of the SARS-coronavirus
              Unpublished
REFERENCE     2 (bases 1 to 29646)
              The SARS epidemiology consortium of Guangdong
              Direct Submission
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              From independent foci of epidemic outbreak to large genomic
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REFERENCE     2 (bases 1 to 29647)

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REFERENCE	1 (bases 1 to 29699)					
AUTHORS	The SARS epidemiology consortium of Guangdong					
CNSTRM	From independent foci of epidemic outbreak to large genomic					
TITLE	alteration in late phase viruses: evolution of the SARS-coronavirus					
JOURNAL	Unpublished					
REFERENCE	2 (bases 1 to 29699)					
AUTHORS	The SARS epidemiology consortium of Guangdong					
CNSTRM	Direct Submission					
TITLE	Submitted (19-SEP-2003) Guangdong, China					
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REFERENCE		1 (bases 1 to 29705)	
AUTHORS		Ruan, Y., Wei, C. L., Ling, A. E., Vega, V. B., Thoreau, H., Se Thoe, S. Y.,	
		Chia, J. -M., Ng, P., Chiu, K. P., Lim, L., Zhang, T., Chan, K. P.,	
		Con, L. E. L., Ng, M. B., Leo, S. Y., Ng, L. F. P., Ren, E. C., Stanton, L. W.,	
		Long, P. M. and Liu, E. T.	
TITLE		Comparative full-length genome sequence analysis of 14 SARS	
		coronavirus isolates and common mutations associated with putative	
		origins of infection	

REMARKS
REFERENCE
Erratum in: *Lancet*. 2003 May 24;361(9371):1832.
2 (bases 1 to 29705)
AUTHORS
Wei, C.L., Thoreau, H., Chia, J.-M., Chiu, K.P., Ng, P., Lim, L.,
Lambert, E., Zhang, T., Wong, M., Se Thoe, S.Y., Chan, K.P. and Ruan, Y.
Direct Submission
TITLE
JOURNAL
Submitted (27-APR-2003) Genome Institute of Singapore, 1 Science

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